

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 15, 2005, 13:56:25 ; Search time 170 Seconds
(without alignments)
1012.402 Million cell updates/sec

Title: US-10-803-156-7

Perfect score: 2256

Sequence: 1 AGAEVVLDPPIKISGVVL.....GCTRTKPPDPVLSFVN 445

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

A_Geneseq_16Dec04:*
1: geneseq19808:*
2: geneseq19908:*
3: geneseq20008:*
4: geneseq20018:*
5: geneseq20028:*
6: geneseq20038:*
7: geneseq20038:*
8: geneseq20048:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2256	100.0	445	AAE09792	Aae09792 Eleusine
2	2199.5	97.5	444	AAW27301	Aaw27301 Maize 5-e
3	2199.5	97.5	444	AAW28461	Aaw28461 Maize 5-e
4	2199.5	97.5	444	AAW44824	Aaw44824 Mutant ma
5	2199.5	97.5	444	AAW4871	Aab67871 5-enolpyr
6	2199.5	97.5	444	ADR67918	Adr67918 wild type
7	2199.5	97.5	444	ADR67921	Adr67921 wild type
8	2198.5	97.5	444	AAW27302	Aaw27302 Maize 5-e
9	2198.5	97.5	444	AAW28462	Aaw28462 Maize 5-e
10	2198.5	97.5	444	AAW44825	Aaw44825 Mutant ma
11	2198.5	97.5	506	ADJ79601	Adj79601 Corn BPSP
12	2187.5	97.0	444	AAW70529	Aaw70529 Mutant ma
13	2187.5	97.0	444	AAW28463	Aaw28463 Maize 5-e
14	2165.5	96.0	444	AAW23065	Aaw23065 Modified
15	2165	96.0	511	ADQ37121	Adq37121 Cell prol
16	2165	96.0	511	ADQ15707	Adq15707 Rice bte
17	2164	95.9	515	ADJ79594	Adj79594 Rice EPSP
18	2130.5	94.4	442	AAW27802	Aaw27802 BPSP synt
19	1927	85.4	448	ADR67919	Adr67919 wild type
20	1927	85.4	516	AAW85136	Aaw85136 A Petunia
21	1927	85.4	516	AAW87870	Aab67870 5-enolpyr
22	1920	85.1	516	AAW32774	Aaw32774 Petunia B
23	1911	84.7	516	AAW85137	Aaw85137 Brasica
24	1911	84.7	516	AAW67869	Aab67869 5-enolpyr
25	1905	84.4	444	AAW23061	Aaw23061 Modified

26	1902	84.3	451	8	ADR67920	Adr67920 wild type
27	1901	84.3	452	3	AAW36512	Aag36512 Arabidops
28	1901	84.3	465	3	AAW40465	Aag40465 Arabidops
29	1901	84.3	520	3	AAW40464	Aag40464 Arabidops
30	1901	84.3	520	5	ABW92125	Abw92125 Herbicida
31	1901	84.3	578	3	AAW40463	Aag40463 Arabidops
32	1899.5	84.2	443	2	AAW27798	Aaw27798 BPSP synt
33	1897	84.1	521	6	ABW39998	Abw39998 A. thalia
34	1894	84.0	525	8	ADJ79598	Adj79598 Soybean B
35	1893	83.9	464	3	AAW34722	Aag34722 Arabidops
36	1893	83.9	521	3	AAW34721	Aag34721 Arabidops
37	1888	83.7	520	4	AAW67847	Aab67847 5-enolpyr
38	1885.5	83.6	445	2	AAW27800	Aaw27800 BPSP synt
39	1879	83.3	444	2	AAW23063	Aaw23063 Modified
40	1871.5	83.0	446	2	AAW23064	Aaw23064 Modified
41	1867	82.8	444	2	AAW23062	Aaw23062 Modified
42	1863.5	82.6	440	2	AAW27799	Aaw27799 BPSP synt
43	1843.5	81.7	496	2	AAW27801	Aaw27801 BPSP synt
44	1682	74.6	391	3	AAW36513	Aag36513 Arabidops
45	1674	74.2	391	3	AAW34723	Aag34723 Arabidops

ALIGNMENTS

RESULT 1	
AAE09792	AAE09792 standard; protein; 445 AA.
AAE09792;	
29-NOV-2001	(first entry)
Eleusine indica BPSP synthase mature protein.	
Goose grass; glyphosate herbicide; N-phosphonomethylglycine; BPSPs;	
5-enolpyruvylshikimate-3-phosphate synthase; phosphoenolpyruvate; PEP;	
transgenic plant.	
Eleusine indica.	
WO200166704-A2.	
13-SEP-2001.	
06-MAR-2001; 2001WO-US007135.	
09-MAR-2000; 2000US-0188093P.	
(MONS) MONSANTO TECHNOLOGY LLC.	
Baerson SR, Heck GJ, Rodriguez DJ;	
WPI; 2001-557661/62.	
N-PSDB; AAD16837.	
Novel DNA molecule encoding naturally occurring glyphosate resistant 5-	
enolpyruvylshikimate-3-phosphate synthase enzyme derived from glyphosate	
tolerant plant species useful for producing glyphosate tolerant plants.	
Claim 5; Fig 2; 69pp; English.	
The patent discloses methods and compositions for making plants tolerant	
to glyphosphate (N-phosphonomethylglycine) herbicide. The invention	
relates to novel glyphosate resistant 5-enolpyruvylshikimate-3-phosphate	
synthase (BPSPs) enzyme from Eleusine indica (goose grass), where the	
enzyme has a K.m for phosphoenolpyruvate (PEP) of less than 10 M. BPSPs	
genes are useful for producing glyphosate tolerant transgenic plants by	
inserting BPSPs gene into the genome of a plant cell, obtaining a	
transformed plant cell, and regenerating from the transformed plant cell	
a genetically transformed plant which has increased tolerance to	
glyphosate herbicide. The present sequence is BPSP synthase mature	
protein from Eleusine indica	

XX Sequence 445 AA;
 SO Query Match 100.0%; Score 2256; DB 4; Length 445;
 Best Local Similarity 100.0%; Pred. No. 2.3e-193;
 Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAEEVVLQPIKEISGVVVKPGSKSLNSRIILLSALAEGLTVVDNLNSEDVHYMLGALK 60
 DB 1 AGAEEVVLQPIKEISGVVVKPGSKSLNSRIILLSALAEGLTVVDNLNSEDVHYMLGALK 60
 QY 61 TLGLSVLEADKAKRAVAVVGGCGKFPVEKDAAKEEVQLFLGNACTAMRSITPAVTAAGNAT 120
 DB 61 TLGLSVLEADKAKRAVAVVGGCGKFPVEKDAAKEEVQLFLGNACTAMRSITPAVTAAGNAT 120
 QY 121 YVLDCVPRMRERPIGDLVVLKQLGADVDCFLGTDCPPRVKIGLPGSKYKLSGSIS 180
 DB 121 YVLDCVPRMRERPIGDLVVLKQLGADVDCFLGTDCPPRVKIGLPGSKYKLSGSIS 180
 QY 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSMRPFYIKGGQ 240
 DB 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSMRPFYIKGGQ 240
 QY 241 KYKSPKNAVVEGDASSASYFLAGAAITGGTVVEGCGTTSLOGDVKFAEVLBMGAKVTM 300
 DB 241 KYKSPKNAVVEGDASSASYFLAGAAITGGTVVEGCGTTSLOGDVKFAEVLBMGAKVTM 300
 QY 301 TETSVTVTGPPREPGRKHLKAI DVNMNMKMPDVAMTLAVVALPADGPTAIRDVASRRVKE 360
 DB 301 TETSVTVTGPPREPGRKHLKAI DVNMNMKMPDVAMTLAVVALPADGPTAIRDVASRRVKE 360
 QY 361 TERMVAIIRTELTKLGSVVEGLDYCIITPPEKLNVTAIIDTYDDHRMAMAFSLAACADVEV 420
 DB 361 TERMVAIIRTELTKLGSVVEGLDYCIITPPEKLNVTAIIDTYDDHRMAMAFSLAACADVEV 420
 QY 421 TIRDPGCTRKTPPDYFDVLSTFVK 445
 DB 421 TIRDPGCTRKTPPDYFDVLSTFVK 445

RESULT 2
 AAW27301
 ID AAW27301 standard; protein; 444 AA.
 AC AAW27301;
 XX
 DT 17-OCT-2003 (revised)
 DT 17-NOV-1997 (first entry)
 XX
 DE Maize 5-enolpyruvylshikimate-3-phosphate synthase.
 XX
 KM plant expression regulation sequence; intron; histone; BPSPS;
 KM 5-enolpyruvylshikimate-3-phosphate synthase; wild-type; corn;
 KM herbicide tolerance; glyphosate; gRPA-MU-715; gRPA-MU-716.
 OS Zea mays; (strain Black Mexican Sweet).
 OS
 XX
 PN WO9704114-A2.
 XX
 PD 06-FEB-1997.
 PD
 XX
 PF 17-JUL-1996; 96MO-FR001109.
 PF
 XX
 PR 19-JUL-1995; 95FR-00008980.
 PR
 XX
 PA (RHON) RHONE POULENC AGROCHIMIE.
 PA
 XX
 PI Deroose R, Chaubet N, Gigot C;
 PI
 XX
 DR WPI; 1997-132652/12.
 DR
 XX
 DR N-PSDB; AAT85994.
 DR
 XX
 PT New regulatory sequence for chimeric gene expression in rapidly growing

PT parts of a plant - includes at least one intron from a plant histone gene
 PT and is useful for imparting resistance to herbicides.
 PS Example 1; Page 22; 31pp; French.
 XX
 XX A 204 bp fragment of the 5-enolpyruvylshikimate-3-phosphate synthase
 CC (EPSPS) gene) was amplified from total DNA of Arabidopsis thaliana (var.
 CC Columbia) using PCR primers having the sequences given in AAT85991 and
 CC AAT85992. Using the amplified fragment as a probe, the wild-type EPSPS
 CC gene was isolated from a maize BMS cDNA library. The EPSPS gene can be
 CC mutated to increase a plant's tolerance to certain herbicides, including
 CC glyphosate. The mutated gene is incorporated into an expression vector
 CC containing a plant promoter and an intron sequence derived from the 5'-
 CC non-coding region of a plant histone gene. The intron enhances expression
 CC of the herbicide tolerance gene in rapidly growing parts of plants. The
 CC intron can also be used to enhance expression of genes that impart
 CC resistance to pathogens or that encode nutritional or therapeutic
 CC proteins. The present sequence represents the wild-type maize EPSPS
 CC enzyme. (Updated on 17-OCT-2003 to standardise OS field)
 XX
 SO Sequence 444 AA;
 Query Match 97.5%; Score 2199.5; DB 2; Length 444;
 Best Local Similarity 97.5%; Pred. No. 2.7e-188;
 Matches 434; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

QY 1 AGAEEVVLQPIKEISGVVVKPGSKSLNSRIILLSALAEGLTVVDNLNSEDVHYMLGALK 60
 DB 1 AGAEEVVLQPIKEISGVVVKPGSKSLNSRIILLSALAEGLTVVDNLNSEDVHYMLGALK 60
 QY 61 TLGLSVLEADKAKRAVAVVGGCGKFPVEKDAAKEEVQLFLGNACTAMRSITPAVTAAGNAT 120
 DB 61 TLGLSVLEADKAKRAVAVVGGCGKFPVEKDAAKEEVQLFLGNACTAMRSITPAVTAAGNAT 119
 QY 121 YVLDCVPRMRERPIGDLVVLKQLGADVDCFLGTDCPPRVKIGLPGSKYKLSGSIS 180
 DB 121 YVLDCVPRMRERPIGDLVVLKQLGADVDCFLGTDCPPRVKIGLPGSKYKLSGSIS 179
 QY 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSMRPFYIKGGQ 240
 DB 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSMRPFYIKGGQ 239
 QY 241 KYKSPKNAVVEGDASSASYFLAGAAITGGTVVEGCGTTSLOGDVKFAEVLBMGAKVTM 300
 DB 241 KYKSPKNAVVEGDASSASYFLAGAAITGGTVVEGCGTTSLOGDVKFAEVLBMGAKVTM 299
 QY 301 TETSVTVTGPPREPGRKHLKAI DVNMNMKMPDVAMTLAVVALPADGPTAIRDVASRRVKE 360
 DB 301 TETSVTVTGPPREPGRKHLKAI DVNMNMKMPDVAMTLAVVALPADGPTAIRDVASRRVKE 359
 QY 361 TERMVAIIRTELTKLGSVVEGLDYCIITPPEKLNVTAIIDTYDDHRMAMAFSLAACADVEV 420
 DB 361 TERMVAIIRTELTKLGSVVEGLDYCIITPPEKLNVTAIIDTYDDHRMAMAFSLAACADVEV 419
 QY 421 TIRDPGCTRKTPPDYFDVLSTFVK 445
 DB 421 TIRDPGCTRKTPPDYFDVLSTFVK 444

RESULT 3
 AAW28461
 ID AAW28461 standard; protein; 444 AA.
 AC AAW28461;
 XX
 DT 17-OCT-2003 (revised)
 DT 17-NOV-1997 (first entry)
 XX
 DE Maize 5-enolpyruvylshikimate-3-phosphate synthase.
 XX
 KM 5-enolpyruvylshikimate-3-phosphate synthase; EPSPS; wild-type; corn;
 KM herbicide tolerance; glyphosate; gRPA-MU-716.
 KM
 XX
 PT

OS Zea mays; (strain Black Mexican Sweet).
 XX
 PN MO9704103-A2.
 XX
 PD 06-FEB-1997.
 XX
 PF 18-JUL-1996; 96MO-FR001125.
 XX
 PR 19-JUL-1995; 95FR-00008979.
 XX
 PA (RHON) RHONE-POULENC AGROCHIMIE.
 XX
 PI Lebrun M., Salland A., Freyestinet G,
 XX
 DR WPI, 1997-132642/12.
 XX
 DR N-PSDB; AAT86001.
 XX
 PT New mutant gene for 5-enol pyruvyl:shikimate-3-phosphate synthase -
 PT encodes an enzyme in which ile replaces thr at position 102 to give
 PT increased tolerance for glyphosate and related herbicides.

PS Example 1; Page 19-20; 26pp; French.

XX A 204 bp fragment of the 5-enolpyruvyl:shikimate-3-phosphate synthase
 CC (EPSPS) gene was amplified from total DNA of Arabidopsis thaliana (var.
 CC Columbia) using PCR primers having the sequences given in AAT85998 and
 CC AAT85999. Using the amplified fragment as a probe, the wild-type EPSPS
 CC gene was isolated from a maize (strain Black Mexican Sweet) cDNA library.
 CC The EPSPS gene can be mutated to increase a plant's tolerance to certain
 CC herbicides, including glyphosate. The present sequence represents the
 CC wild-type maize EPSPS enzyme. Claimed mutant genes encode EPSPS in which
 CC at least wild-type Thr at position 102 has been replaced by Ile.
 CC Additional mutations are of Pro at position 106 to Ser and Gly at
 CC position 101 to Ala. (Updated on 17-Oct-2003 to standardise OS field)

XX Sequence 444 AA;

XX Query Match 97.5%; Score 2199.5; DB 2; Length 444;

XX Best Local Similarity 97.5%; Pred. No. 2.7e-188;

XX Matches 434; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

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QY 1 AGAEEVVLQPIKEISGVVGLPGSKSLSNRIILLSALAEQTVVDNLINSEDVHYMLGALK 60
DB 1 AGAEEVVLQPIKEISGVVGLPGSKSLSNRIILLSALAEQTVVDNLINSEDVHYMLGALK 60
QY 61 TGLSVADKAAKRAVAVVGGCGKFPVE-DAKEEVQLFLGNAGTAMRPLTAATAAGNAT 120
DB 61 TGLSVADKAAKRAVAVVGGCGKFPVE-DAKEEVQLFLGNAGTAMRPLTAATAAGNAT 119
QY 121 VYLDGVPRRRERIRIGLVVGLKQLGADVDFLGTDCPPRVKIGLPGSKVLSGSISS 180
DB 121 VYLDGVPRRRERIRIGLVVGLKQLGADVDFLGTDCPPRVKIGLPGSKVLSGSISS 179
QY 120 VYLDGVPRRRERIRIGLVVGLKQLGADVDFLGTDCPPRVKIGLPGSKVLSGSISS 179
DB 120 VYLDGVPRRRERIRIGLVVGLKQLGADVDFLGTDCPPRVKIGLPGSKVLSGSISS 179
QY 181 QYLSALLMAAPLALGVVEIRIIDKLSIPYVENTLILMERFGVKAHSHSMDRFFYKGGQ 240
DB 181 QYLSALLMAAPLALGVVEIRIIDKLSIPYVENTLILMERFGVKAHSHSMDRFFYKGGQ 239
QY 180 QYLSALLMAAPLALGVVEIRIIDKLSIPYVENTLILMERFGVKAHSHSMDRFFYKGGQ 239
DB 180 QYLSALLMAAPLALGVVEIRIIDKLSIPYVENTLILMERFGVKAHSHSMDRFFYKGGQ 239
QY 241 KYKSPKNAAYVEGDASASYFLAGAAITGGTVVEGGCTSLQGVKFAVLEMMGAKVTM 300
DB 240 KYKSPKNAAYVEGDASASYFLAGAAITGGTVVEGGCTSLQGVKFAVLEMMGAKVTM 299
QY 301 TETSIVTGPORPPRRKRLKALDVNMNKKPDMVAMTLAVVALFADGPTAIRDVASRVKE 360
DB 300 TETSIVTGPORPPRRKRLKALDVNMNKKPDMVAMTLAVVALFADGPTAIRDVASRVKE 359
QY 361 TERHVAIRTELTDGASVEBGLDYCIITPEPKLNTAIDTYDHRMAAFSLAACADVRY 420
DB 360 TERHVAIRTELTDGASVEBGLDYCIITPEPKLNTAIDTYDHRMAAFSLAACADVRY 419
QY 421 TIRDPGCTRTKTPDYFDVLSFVKN 445
DB 420 TIRDPGCTRTKTPDYFDVLSFVKN 444

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RESULT 4

AAW44824 standard; protein; 444 AA.

AAW44824;

23-NOV-1998 (first entry)

Mutant maize EPSPS encoded by clone pRPA-MU-716.

Transgenic plant; resistance: herbicide; chimaeric gene; tolerance; PCR;
 hydroxyphenylpyruvate dioxygenase; isoxaflutole; sulcotriene; primer;
 amplification; tobacco; cotton; rape; soy; sugar beet; cereal; ioxynil;
 nitrilase; dihalohydroxybenzonitrile; bromoxynil; nematode; insecticide;
 glyphosate oxidoreductase; Bacillus thuringiensis; fungus; maize; EPSPS;
 5-enolpyruvyl-3-phosphoshikimate synthase.

Zea mays.

MO9802562-A2.

22-JAN-1998.

10-JUL-1997; 97MO-FR001256.

16-JUL-1996; 96FR-00009137.

(RHON) RHONE-POULENC AGROCHIMIE.

Pallett K., Deroose R., Pellissier B., Salland A;

WPI, 1998-110608/10.

N-PSDB; AAV19278.

Chimaeric gene imparting resistance to two or more herbicides - such as
 hydroxyphenylpyruvate dioxygenase inhibitors, also related vectors and
 transformed plants.

Example 2; Page 31-32; 49pp; French.

The invention relates to the generation of transgenic plants resistant to
 preferably at least 2 herbicides by introducing a chimaeric gene
 comprising at least 2 gene subunits where one sequence encodes
 hydroxyphenylpyruvate dioxygenase (HPPD), an enzyme that promotes
 tolerance to herbicides such as isoxaflutole or sulcotriene (see
 AAV19269). The plants, e.g. tobacco, cotton, rape, soy, sugar beet,
 cereals, may also contain a gene encoding e.g. a nitrilase for resistance
 to dihalohydroxybenzonitriles such as bromoxynil or ioxynil, glyphosate
 oxidoreductase for resistance to glyphosate. This sequence represents the
 maize 5-enolpyruvyl-3-phosphoshikimate synthase (EPSPS). The coding
 sequence contains a mutation in which the NcoI site at position 1217 is
 destroyed by site directed mutagenesis, which is a silent mutation and
 does not affect the sequence of the encoded protein. A third gene
 encoding a Bacillus thuringiensis insecticidal protein or proteins
 imparting resistance to fungi or nematodes, may also be introduced into
 the plant

Sequence 444 AA;

Query Match 97.5%; Score 2199.5; DB 2; Length 444;

Best Local Similarity 97.5%; Pred. No. 2.7e-188;

Matches 434; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

```

QY 1 AGAEEVVLQPIKEISGVVGLPGSKSLSNRIILLSALAEQTVVDNLINSEDVHYMLGALK 60
DB 1 AGAEEVVLQPIKEISGVVGLPGSKSLSNRIILLSALAEQTVVDNLINSEDVHYMLGALK 60
QY 61 TGLSVADKAAKRAVAVVGGCGKFPVEKDAKEEVQLFLGNAGTAMRSLTAATAAGNAT 120
DB 61 TGLSVADKAAKRAVAVVGGCGKFPVE-DAKEEVQLFLGNAGTAMRPLTAATAAGNAT 119
QY 121 VYLDGVPRRRERIRIGLVVGLKQLGADVDFLGTDCPPRVKIGLPGSKVLSGSISS 180

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|||||
Db      120 YVLGVPKRRERPIGDLVVGKQLGADVDFLGTDCCPVRVNGIGLPGKVKLSGSIS 179
Qy      181 QYLSALLMAAPLALGDVEIEIIDKLSIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
Db      180 QYLSALLMAAPLALGDVEIEIIDKLSIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQ 239
Qy      241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVVEGCGTTSLOGDVKFAEVLMMGAKVTM 300
Db      240 KYKSPKNAYVEGDASSASYFLAGAAITGGTVVEGCGTTSLOGDVKFAEVLMMGAKVTM 299
Qy      301 TETSVTYTGPOREPFGRRKHLKAIDVNMNKMPPDVAMTLAVVALPADGPTAIRDVASRWYK 360
Db      300 TETSVTYTGPOREPFGRRKHLKAIDVNMNKMPPDVAMTLAVVALPADGPTAIRDVASRWYK 359
Qy      361 TERMWAIRTELTKLGASVEEGDYCIITPEKLVNTAIDTYDDHRMAMFSLAACADVPV 420
Db      360 TERMWAIRTELTKLGASVEEGDYCIITPEKLVNTAIDTYDDHRMAMFSLAACADVPV 419
Qy      421 TIRDPGCTRKTPFDYFDVLTSTFVN 445
Db      420 TIRDPGCTRKTPFDYFDVLTSTFVN 444

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RESULT 5
AAB67871 standard; protein; 444 AA.

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XX AC      AAB67871;
XX DT      29-JUN-2001 (first entry)
XX DE      5-enolpyruvylshikimate-3-phosphate synthase (EPSPS) polypeptide.
XX OS      Zea mays.
XX PN      MO200124615-A1.
XX PD      12-APR-2001.
XX PF      10-OCT-2000; 2000MO-US027941.
XX PR      07-OCT-1999; 99US-0158027P.
XX RA      30-DEC-1999; 99US-0173564P.
XX (VALI-) VALIGEN US INC.
XX PI      Beetham PR, Avlasar PL, Walker KA, Metz RA;
XX DR      WPI; 2001-273533/28.
XX PT      Novel non-transgenic herbicide resistant plant expressing mutant 5-
XX PT      enolpyruvylshikimate-3-phosphate synthase and the enzyme, plant retain
XX PT      catalytic activity and growth of wild-type gene product.
XX PS      Disclosure; Fig 4; 5pp; English.

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The present sequence represents a 5-enolpyruvylshikimate-3-phosphate synthase (EPSP synthase or EPSPs). The specification describes a non-transgenic herbicide resistant plant which expresses a mutant EPSPs gene product which has substantially the same level of catalytic activity as compared to the wild-type gene product, and which plant has substantially normal growth as compared to a plant expressing the wild-type EPSPs gene product. The mutated EPSPs protein allows for increased resistance or tolerance of a plant to the herbicide of the phosphonemethyl glycine family and allows for substantially normal growth or development of the plant, its organs, tissues or cells as compared to the wild-type plant irrespective of the presence or absence of the herbicide. The EPSPs is used in the production of non-transgenic herbicide (glyphosate) resistant plants such as corn, wheat, rice, barley, soybean, cotton, sugarbeet.

CC oilseed rape, canola, flax, sunflower, potato, tobacco, tomato, alfalfa, CC poplar, pine, eucalyptus, apple, lettuce, peas, lentils, grape, turf CC grass or Brassica sp

XX SQ Sequence 444 AA;

Query Match 97.5%; Score 2199.5; DB 4; Length 444;
Best Local Similarity 97.5%; Pred. No. 2.7e-188;
Matches 434; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

```

Qy      1 AGAEVYVLOPIKEIGGVKTLPGSKLSNRILLLSLAEGTIVYNDLNSEDVHYMLGALK 60
Db      1 AGAEVIVLOPIKEIGGVKTLPGSKLSNRILLLSLAEGTIVYNDLNSEDVHYMLGALK 60
Qy      61 TLGLSVEADKAKRAVWVGCGGKFPVEKDAKEEVOLPIGNAGTAMRSILTAATAAGNAT 120
Db      61 TLGLSVEADKAKRAVWVGCGGKFPVE-DAKEEVOLFIENAGTAMRPLTAATAAGNAT 119
Qy      121 YVLGVPKRRERPIGDLVVGKQLGADVDFLGTDCCPVRVNGIGLPGKVKLSGSIS 180
Db      120 YVLGVPKRRERPIGDLVVGKQLGADVDFLGTDCCPVRVNGIGLPGKVKLSGSIS 179
Qy      181 QYLSALLMAAPLALGDVEIEIIDKLSIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
Db      180 QYLSALLMAAPLALGDVEIEIIDKLSIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQ 239
Qy      241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVVEGCGTTSLOGDVKFAEVLMMGAKVTM 300
Db      240 KYKSPKNAYVEGDASSASYFLAGAAITGGTVVEGCGTTSLOGDVKFAEVLMMGAKVTM 299
Qy      301 TETSVTYTGPOREPFGRRKHLKAIDVNMNKMPPDVAMTLAVVALPADGPTAIRDVASRWYK 360
Db      300 TETSVTYTGPOREPFGRRKHLKAIDVNMNKMPPDVAMTLAVVALPADGPTAIRDVASRWYK 359
Qy      361 TERMWAIRTELTKLGASVEEGDYCIITPEKLVNTAIDTYDDHRMAMFSLAACADVPV 420
Db      360 TERMWAIRTELTKLGASVEEGDYCIITPEKLVNTAIDTYDDHRMAMFSLAACADVPV 419
Qy      421 TIRDPGCTRKTPFDYFDVLTSTFVN 445
Db      420 TIRDPGCTRKTPFDYFDVLTSTFVN 444

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RESULT 6
ADR67918 standard; protein; 444 AA.

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XX AC      ADR67918;
XX DT      18-NOV-2004 (first entry)
XX DE      Wild type EPSPs from maize.
XX OS      Zea mays.
XX PN      WO2004074443-A2.
XX PD      02-SEP-2004.
XX PF      17-FEB-2004; 2004MO-US004636.
XX PR      18-FEB-2003; 2003US-0449438P.
XX RA      (MONS ) MONSANTO TECHNOLOGY LLC.
XX PI      Alibhai MF, Cajacob C, Feng PCC, Heck GR, Qi Y, Flaasink S;
XX PT      Stallings WC;

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DR WPI; 2004-635563/61.
 DR N-PSDB; ADR67921.
 XX
 PT New isolated DNA molecule that encodes a glyphosate resistant class I 5-enolpyruvylshikimate-3-phosphate synthase (EPSPS) protein, useful for
 PT preparing glyphosate tolerant plants.
 XX
 PS Example 1; Fig 1; 73pp; English.
 XX
 CC This sequence is encoded by an isolated DNA molecule that encodes a
 CC glyphosate resistant class I 5-enolpyruvylshikimate-3-phosphate synthase
 CC (EPSPS) protein. A variant of this sequence may be used in the method of
 CC the invention for preparing a glyphosate tolerant plant. The method
 CC comprises contacting a recipient plant cell with a DNA construct
 CC comprising the EPSPS sequence under the control of a plant specific
 CC promoter, that is incorporated into the genome of the recipient plant
 CC cell; regenerating the recipient plant cell into a plant; and applying an
 CC effective dose of glyphosate to the plant, where the plant displays a
 CC glyphosate tolerant phenotype. The resulting plants may be used in a
 CC method of controlling weeds in a field of glyphosate tolerant crop plants
 CC by applying to the field of glyphosate tolerant crop plant an effective
 CC dose of a glyphosate containing herbicide.
 CC
 SQ Sequence 444 AA;

Query Match 97.5%; Score 2199.5; DB 8; Length 444;
 Best Local Similarity 97.5%; Pred. No. 2.7e-188;

Matches 434; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

QY 1 AGAEEVVLQPIKEISGVVTLPGSKSLSNRIILLSALAEETTVNDNLNSEDVHYMLGALK 60
 DB 1 AGAEEVILQPIKEISGVVTLPGSKSLSNRIILLSALAEETTVNDNLNSEDVHYMLGALK 60
 QY 61 TLGLSVADKAKRAVAVVCGGKFPVEKDAKEEVQLFLNAGTAMRSLTAATTAAGGNAT 120
 DB 61 TLGLSVADKAKRAVAVVCGGKFPVE-DAKEEVQLFLNAGTAMRPLTAATTAAGGNAT 119
 QY 121 YVLDGVPKRRERPIGDLVVLGKQLGADVDCFLGDCPPRVKNGIGLPGSKVXLSGSISS 180
 DB 120 YVLDGVPKRRERPIGDLVVLGKQLGADVDCFLGDCPPRVKNGIGLPGSKVXLSGSISS 179
 QY 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFVKAEHSDMSDFYIKGGQ 240
 DB 180 QYLSALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFVKAEHSDMSDFYIKGGQ 239
 QY 241 KYKSPKNAVVEGDASASVFLAGAAITGCTVVEGCGTISLQGDVKAFAVLEMMGAKVTW 300
 DB 240 KYKSPKNAVVEGDASASVFLAGAAITGCTVVEGCGTISLQGDVKAFAVLEMMGAKVTW 299
 QY 301 TETSVTVTGPORPFRGKRLKALDVNNMKMPDVAMTLAVVALPADGPTAIRDVASWRVKE 360
 DB 300 TETSVTVTGPORPFRGKRLKALDVNNMKMPDVAMTLAVVALPADGPTAIRDVASWRVKE 359
 QY 361 TERHVAIRTELTLGLASVEEGLDYCIITPEKLTNTAIDTYDDHRMAMAFSLAACADVPY 420
 DB 360 TERHVAIRTELTLGLASVEEGDPYCIITPEKLTNTAIDTYDDHRMAMAFSLAACAEVY 419
 QY 421 TIRDPGCTKRTFPDYEDVLTSTFYKN 445
 DB 420 TIRDPGCTKRTFPDYEDVLTSTFYKN 444

RESULT 7
 ADR67921
 ID ADR67921 standard; protein; 444 AA.
 AC ADR67921;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Wild type EPSPS from maize.
 XX
 KW glyphosate resistant; class I;

KW 5-enolpyruvylshikimate-3-phosphate synthase; EPSPS; T1021; P106A; T1PA;
 KW mutation; glyphosate tolerant plant; glyphosate; weed control; herbicide;
 KW transgenic; plant.
 XX
 XX
 OS Petunia sp.
 XX
 PN WO2004074443-A2.
 XX
 PD 02-SBP-2004.
 XX
 PF 17-FEB-2004; 2004WO-US004636.
 XX
 PR 18-FEB-2003; 2003US-0448438P.
 XX
 PA (MONS) MONSANTO TECHNOLOGY LLC.
 XX
 PI Alibhai MF, CaJacob C, Feng PCC, Heck GR, Qi Y, Plasinski S;
 PI Stallings WC;
 XX
 DR WPI; 2004-635563/61.
 XX
 PT New isolated DNA molecule that encodes a glyphosate resistant class I 5-enolpyruvylshikimate-3-phosphate synthase (EPSPS) protein, useful for
 PT preparing glyphosate tolerant plants.
 XX
 PS Example 1; Fig 2; 73pp; English.

Query Match 97.5%; Score 2199.5; DB 8; Length 444;
 Best Local Similarity 97.5%; Pred. No. 2.7e-188;

Matches 434; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

QY 1 AGAEEVVLQPIKEISGVVTLPGSKSLSNRIILLSALAEETTVNDNLNSEDVHYMLGALK 60
 DB 1 AGAEEVILQPIKEISGVVTLPGSKSLSNRIILLSALAEETTVNDNLNSEDVHYMLGALK 60
 QY 61 TLGLSVADKAKRAVAVVCGGKFPVEKDAKEEVQLFLNAGTAMRSLTAATTAAGGNAT 120
 DB 61 TLGLSVADKAKRAVAVVCGGKFPVE-DAKEEVQLFLNAGTAMRPLTAATTAAGGNAT 119
 QY 121 YVLDGVPKRRERPIGDLVVLGKQLGADVDCFLGDCPPRVKNGIGLPGSKVXLSGSISS 180
 DB 120 YVLDGVPKRRERPIGDLVVLGKQLGADVDCFLGDCPPRVKNGIGLPGSKVXLSGSISS 179
 QY 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFVKAEHSDMSDFYIKGGQ 240
 DB 180 QYLSALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFVKAEHSDMSDFYIKGGQ 239
 QY 241 KYKSPKNAVVEGDASASVFLAGAAITGCTVVEGCGTISLQGDVKAFAVLEMMGAKVTW 300
 DB 240 KYKSPKNAVVEGDASASVFLAGAAITGCTVVEGCGTISLQGDVKAFAVLEMMGAKVTW 299
 QY 301 TETSVTVTGPORPFRGKRLKALDVNNMKMPDVAMTLAVVALPADGPTAIRDVASWRVKE 360
 DB 300 TETSVTVTGPORPFRGKRLKALDVNNMKMPDVAMTLAVVALPADGPTAIRDVASWRVKE 359
 QY 361 TERHVAIRTELTLGLASVEEGLDYCIITPEKLTNTAIDTYDDHRMAMAFSLAACADVPY 420

RESULT 7
 ADR67921
 ID ADR67921 standard; protein; 444 AA.
 AC ADR67921;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Wild type EPSPS from maize.
 XX
 KW glyphosate resistant; class I;

```

Db      360  TERMAAIRTELTKLGASVEEGPDYCIITPEKLNVTALDITDDHRMAMFSLAACAEVVP 419
QY      421  TIRDPGCTRKTEPPDYFDVLSTFVK 445
Db      420  TIRDPGCTRKTEPPDYFDVLSTFVK 444

RESULT 8
AAW27302
ID      AAW27302 standard; protein; 444 AA.
AC      AAW27302;
DT      17-NOV-1997 (first entry)
DE      Maize 5-enolpyruvylshikimate-3-phosphate synthase double mutant.
XX
XX      Plant expression regulation sequence; intron; histone; EPSPS;
KM      5-enolpyruvylshikimate-3-phosphate synthase; wild-type; corn;
KM      herbicide tolerance; glyphosate; pRPA-ML-720.
XX
OS      Zea mays; (strain Black Mexican Sweet).
OS      Synthetic.
FH      Key
FH      M18c-difference 102
FT      M18c-difference /note= "Wild-type Thr has been replaced by Ile"
FT      M18c-difference 106
FT      /note= "Wild-type Pro has been replaced by Ser"
XX
XX      WO9704114-A2.
XX
XX      06-FEB-1997.
XX
XX      17-JUL-1996; 96WO-FR001109.
XX
XX      19-JUL-1995; 95FR-00008980.
XX
XX      (RHON ) RHONE POULENC AGROCHIMIE.
PA
PI      Derose R, Chaubet N, Glogot C;
XX
XX      MPI; 1997-132652/12.
XX      N-PSDB; AAT85995.
XX
XX      New regulatory sequence for chimeric gene expression in rapidly growing
PT      parts of a plant - includes at least one intron from a plant histone gene
PT      and is useful for imparting resistance to herbicides.
XX
XX      Example 1; Page 25; 31pp; French.
XX
XX      A 204 bp fragment of the 5-enolpyruvylshikimate-3-phosphate synthase
CC      (EPSPS) gene) was amplified from total DNA of Arabidopsis thaliana (var.
CC      Columbia) using PCR primers having the sequences given in AAT85991 and
CC      AAT85992. Using the amplified fragment as a probe, the wild-type EPSPS
CC      gene was isolated from a maize BMS CDNA library. The EPSPS gene can be
CC      mutated to increase a plant's tolerance to certain herbicides, including
CC      glyphosate. The present sequence represents a specific example of a EPSPS
CC      double mutant in which the wild-type amino acids at positions 102 and 106
CC      of the enzyme have been changed by site-directed mutagenesis of the EPSPS
CC      gene. The mutated gene is incorporated into an expression vector
CC      containing a plant promoter and an intron sequence derived from the 5'-
CC      non-coding region of a plant histone gene. The intron enhances expression
CC      of the herbicide tolerance gene in rapidly growing parts of plants. The
CC      intron can also be used to enhance expression of genes that impart
CC      resistance to pathogens or that encode nutritional or therapeutic
CC      proteins
XX
XX      Sequence 444 AA:
XX
Query Match      97.5%; Score 2190.5; DB 2; Length 444;
Best Local Similarity 97.5%; Pred. No. 3,4e-188;

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Matches 434; Conservative 5; Mismatches 5; Indels 1; Gaps 1;
QY      1  AGAEEVVOPIKEISGVYKLGSGSKLSNRILLLSALAGTAYVNDLNSEDVHYMGAK 60
Db      1  AGAEEIVLOPIKEISGVYKLGSGSKLSNRILLLSALAGTAYVNDLNSEDVHYMGALR 60
QY      61  TLGLSVEADKAKRAVWVGCGGKFPVEKDAKEVOLFLGNACTAMRSILTAAYTAAGNAT 120
Db      61  TLGLSVEADKAKRAVWVGCGGKFPVE--DAKEVOLFLGNAGIAMRSILTAAYTAAGNAT 119
QY      121  YTLDGVPKRRERPIGDLVYGLKQLGADVDCFLGTCDCPPYRVKVGIGLPGGKYKLSGSISS 180
Db      120  YTLDGVPKRRERPIGDLVYGLKQLGADVDCFLGTCDCPPYRVVNGIGLPGGKYKLSGSISS 179
QY      181  QYLSALMLAAPIALGDVEIEIIDKLSIPYEMTLRLMERPGVKAEHSDSMDFYIKGSG 240
Db      180  QYLSALMLAAPIALGDVEIEIIDKLSIPYEMTLRLMERFGVKAEHSDSMDFYIKGSG 239
QY      241  KYKSPKNAVVEGDASASAYFLAGAAITGGTVVEGCGTTSLOGDYKFAVLEMGAKVTM 300
Db      240  KYKSPKNAVVEGDASASAYFLAGAAITGGTVVEGCGTTSLOGDYKFAVLEMGAKVTM 299
QY      301  TETSVTVTGPPREPGRGHLKAI DVNMNMPPVAMTLAVPALPADGPTAIRDVASRWYKE 360
Db      300  TETSVTVTGPPREPGRGHLKAI DVNMNMPPVAMTLAVPALPADGPTAIRDVASRWYKE 359
QY      361  TERMAAIRTELTKLGASVEEGDYCIITPEKLNVTALDITDDHRMAMFSLAACADVPV 420
Db      360  TERMAAIRTELTKLGASVEEGPDYCIITPEKLNVTALDITDDHRMAMFSLAACAEVVP 419
QY      421  TIRDPGCTRKTEPPDYFDVLSTFVK 445
Db      420  TIRDPGCTRKTEPPDYFDVLSTFVK 444

RESULT 9
AAW28462
ID      AAW28462 standard; protein; 444 AA.
AC      AAW28462;
DT      17-NOV-1997 (first entry)
DE      Maize 5-enolpyruvylshikimate-3-phosphate synthase T1021, P106S mutant.
XX
XX      5-enolpyruvylshikimate-3-phosphate synthase; EPSPS; wild-type; corn;
KM      herbicide tolerance; glyphosate; pRPA-ML-720.
XX
XX      Zea mays; (strain Black Mexican Sweet).
OS      Synthetic.
FH      Key
FH      M18c-difference 102
FT      M18c-difference /note= "Wild-type Thr has been replaced by Ile"
FT      M18c-difference 106
FT      /note= "Wild-type Pro has been replaced by Ser"
XX
XX      WO9704103-A2.
XX
XX      06-FEB-1997.
XX      18-JUL-1996; 96WO-FR001125.
XX
XX      19-JUL-1995; 95FR-00008979.
XX
XX      (RHON ) RHONE POULENC AGROCHIMIE.
PA
PI      Lebrun M, Sailland A, Freysinet G;
XX
XX      MPI; 1997-132642/12.
XX      N-PSDB; AAT86002.
XX
XX      New mutant gene for 5-enol pyruvylshikimate-3-phosphate synthase -
PT

```


XX SO Sequence 570 AA; 97.4%; Score 2196.5; DB 2; Length 570;
 Query Match Best Local Similarity 97.3%; Pred. No. 7.3e-188;
 Matches 433; Conservative 6; Mismatches 5; Indels 1; Gaps 1;

QY 1 AGAEEVVLQPIKISGVVVKLPGSKSLSNRIILLSALAEGETTVVDNLNSEDVHYMGLAK 60
 |||||
 DB 127 AGAEEVVLQPIKISGVVVKLPGSKSLSNRIILLSALAEGETTVVDNLNSEDVHYMGLAK 186
 |||||

QY 61 TLGLSYEADKAAKRAVAVVCGCGKFPVEKDAKEEVQLFLGNAGTAMRSILTAATAAGGNAT 120
 187 TLGLSYEADKAAKRAVAVVCGCGKFPVE-DAKEEVQLFLGNAGTAMRSILTAATAAGGNAT 245

QY 121 YVLIDGVPKRRERPIGDLVVGKQLGADVDCFLGTCDCPPVRVNGIGLPGSKVTLGSGSIS 180
 246 YVLIDGVPKRRERPIGDLVVGKQLGADVDCFLGTCDCPPVRVNGIGLPGSKVTLGSGSIS 305

QY 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSMDRPFYIKGGO 240
 DB 306 QYLSALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSMDRPFYIKGGO 365

QY 241 KYKSPKNAAYVEGDASASASYFLAGAAITGGTVVEGCGTTSLOGDVKFAEVLMMGAKVTM 300
 DB 366 KYKSPKNAAYVEGDASASASYFLAGAAITGGTVVEGCGTTSLOGDVKFAEVLMMGAKVTM 425

QY 301 TETSVTVTGPPQRPFGPKRLKALIDVNMNMMPDVAMTLAVVALPADGPTAIRVVASWRVKE 360
 DB 426 TETSVTVTGPPQRPFGPKRLKALIDVNMNMMPDVAMTLAVVALPADGPTAIRVVASWRVKE 485

QY 361 TERMVAIRTELTKLASVEEGDLYCITTPPEKLNATADITYDDHRMAAFSLAACADVPY 420
 DB 486 TERMVAIRTELTKLASVEEGDLYCITTPPEKLNATADITYDDHRMAAFSLAACADVPY 545

QY 421 TIRDPGCTRKTPPDYFDVLSTFVK 445
 DB 546 TIRDPGCTRKTPPDYFDVLSTFVK 570

RESULT 13
 AAM28463
 ID AAM28463 standard; protein; 444 AA.
 AC AAM28463;
 AC
 DT 17-NOV-1997 (first entry)
 XX
 DE Maize 5-enolpyruvylshikimate-3-phosphate synthase G101A,T102I mutant.
 XX
 KW 5-enolpyruvylshikimate-3-phosphate synthase; EPSPS; wild-type; corn;
 KM herbicide tolerance; glyphosate; pRPA-MT-720.
 XX
 OS Zea mays; (strain Black Mexican Sweet).
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT M18c-difference 101
 FT /note= "Wild-type Gly has been replaced by Ala"
 FT M18c-difference 102
 FT /note= "Wild-type Thr has been replaced by Ile"
 XX
 PN MO9704103-A2.
 XX
 PD 06-FEB-1997.
 XX
 PF 18-JUL-1996; 96MO-FR001125.
 XX
 PR 19-JUL-1995; 95FR-00008979.
 XX
 PA (RHON) RHONE POULENC AGROCHIMIE.
 XX
 PI Lebrun M, Salland A, Freysinet G;

XX DR MPI, 1997-132642/12.
 DR N-PSDB; AAT86003.
 XX
 PT New mutant gene for 5-enol pyruvylshikimate-3-phosphate synthase -
 PT encodes an enzyme in which Ile replaces Thr at position 102 to give
 PT increased tolerance for glyphosate and related herbicides.
 XX
 PS Claim 9; Page; 26pp; French.
 XX
 CC A 204 bp fragment of the 5-enolpyruvylshikimate-3-phosphate synthase
 CC (EPSPS) gene) was amplified from total DNA of Arabidopsis thaliana (var.
 CC Columbia) using PCR primers having the sequences given in AAT85998 and
 CC AAT85999. Using the amplified fragment as a probe, the wild-type EPSPS
 CC gene was isolated from a maize BMS cDNA library. The EPSPS gene can be
 CC mutated to increase a plant's tolerance to certain herbicides, including
 CC glyphosate. The present sequence represents a specifically claimed
 CC example of a EPSPS double mutant in which the wild-type amino acids at
 CC positions 101 and 102 of the enzyme have been changed by site-directed
 CC mutagenesis of the coding sequence (see features table). Note: this
 CC sequence is not given in the specification but has been created by
 CC modifying the wild-type sequence (AAM28461) as described in example 1
 XX

XX SO Sequence 444 AA; 97.0%; Score 2187.5; DB 2; Length 444;
 Query Match Best Local Similarity 97.1%; Pred. No. 3.3e-187;
 Matches 432; Conservative 5; Mismatches 7; Indels 1; Gaps 1;

QY 1 AGAEEVVLQPIKISGVVVKLPGSKSLSNRIILLSALAEGETTVVDNLNSEDVHYMGLAK 60
 |||||
 DB 1 AGAEEVVLQPIKISGVVVKLPGSKSLSNRIILLSALAEGETTVVDNLNSEDVHYMGLAK 60

QY 61 TLGLSYEADKAAKRAVAVVCGCGKFPVEKDAKEEVQLFLGNAGTAMRSILTAATAAGGNAT 120
 DB 61 TLGLSYEADKAAKRAVAVVCGCGKFPVE-DAKEEVQLFLGNAGTAMRSILTAATAAGGNAT 119

QY 121 YVLIDGVPKRRERPIGDLVVGKQLGADVDCFLGTCDCPPVRVNGIGLPGSKVTLGSGSIS 180
 DB 120 YVLIDGVPKRRERPIGDLVVGKQLGADVDCFLGTCDCPPVRVNGIGLPGSKVTLGSGSIS 179

QY 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSMDRPFYIKGGO 240
 DB 180 QYLSALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSMDRPFYIKGGO 239

QY 241 KYKSPKNAAYVEGDASASASYFLAGAAITGGTVVEGCGTTSLOGDVKFAEVLMMGAKVTM 300
 DB 240 KYKSPKNAAYVEGDASASASYFLAGAAITGGTVVEGCGTTSLOGDVKFAEVLMMGAKVTM 299

QY 301 TETSVTVTGPPQRPFGPKRLKALIDVNMNMMPDVAMTLAVVALPADGPTAIRVVASWRVKE 360
 DB 300 TETSVTVTGPPQRPFGPKRLKALIDVNMNMMPDVAMTLAVVALPADGPTAIRVVASWRVKE 359

QY 361 TERMVAIRTELTKLASVEEGDLYCITTPPEKLNATADITYDDHRMAAFSLAACADVPY 420
 DB 360 TERMVAIRTELTKLASVEEGDLYCITTPPEKLNATADITYDDHRMAAFSLAACADVPY 419

QY 421 TIRDPGCTRKTPPDYFDVLSTFVK 445
 DB 420 TIRDPGCTRKTPPDYFDVLSTFVK 444

RESULT 14
 AAR23065
 ID AAR23065 standard; protein; 444 AA.
 AC AAR23065;
 AC
 DT 22-OCT-1992 (first entry)
 XX
 DE Modified 5-enolpyruvyl-3-phosphoshikimate synthetase (5).
 XX
 KM EPSP; Km; phosphoenolpyruvate; chloroplast; CTP.

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XX  Zea mays.
OS  Key
XX  Location/Qualifiers
FH  Misc-difference 98
FT  /note= "glycine mutated to alanine"
FT  188
FT  Misc-difference 188
FT  /label= ALG, SER, THR
FT  /note= "pref Thr"
XX
XX  MO9206201-A.
XX
XX  16-APR-1992.
XX
XX  26-SEP-1991; 91MO-US007068.
XX
XX  28-SEP-1990; 90US-00590647.
XX
XX  (MONS ) MONSANTO CO.
XX
XX  Eichholtz DA, Gasser CS, Kishore GM;
XX  WPI; 1992-150886/18.
XX
XX  Prodn. of glyphosate tolerant plants - comprises transforming plants with
XX  modified 5-enolpyruvyl-3-phosphoshikimate synthase gene.
XX  Disclosure; Fig 1; 87pp; English.
XX
XX  The sequence given encodes a 5-enolpyruvyl-3-phosphoshikimate synthetase
XX  (EPSP) enzyme which exhibits raised tolerance to glyphosate herbicide
XX  while also exhibiting lower Km values for phosphoenolpyruvate than other
XX  variant EPSP synthase enzymes. These changes are effected by the amino
XX  acid changes indicated. The sequence contains conserved regions which can
XX  be seen over a broad evolutionary range. This enzyme encodes a
XX  polypeptide which contains a chloroplast transit peptide (CTP), which
XX  enables the EPSP synthase polypeptide to be transported into a
XX  chloroplast inside the plant cell. The EPSP synthase gene is transcribed
XX  into mRNA in the nucleus and the mRNA is translated into a precursor
XX  polypeptide. This is then transported into the chloroplast at which time
XX  the CTP is cleaved to produce the mature EPSP synthase enzyme
XX
SQ  Sequence 444 AA;

Query Match          96.0%; Score 2165.5; DB 2; Length 444;
Best Local Similarity 96.2%; Pred. No. 3.1e-185;
Matches 428; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

OY  1 AGAEEVVLQPIKEISGVVKKLPGSKSLSNRIILLSALAEGLTVVDNLNSDVHYMLGALK 60
    1 AGAEEIVLQPIKEISGVVKKLPGSKSLSNRIILLSALAEGLTVVDNLNSDVHYMLGALKR 60
DB  1
OY  61 TLGLSVBADKAAKRAVWVGCGGKFPVE-DAKEEVQLFLNAGTAMRPLTAATTAAGNAT 120
    61 TLGLSVBADKAAKRAVWVGCGGKFPVE-DAKEEVQLFLNAGTAMRPLTAATTAAGNAT 119
DB  61
OY  121 YVLGVPKMRERPIGDLVVGKLGADVDFLGTDCPPRVKVGIGLPGSKVYKLSGSIS 180
    121 YVLGVPKMRERPIGDLVVGKLGADVDFLGTDCPPRVKVGIGLPGSKVYKLSGSIS 180
DB  120
OY  120 YVLGVPKMRERPIGDLVVGKLGADVDFLGTDCPPRVKVGIGLPGSKVYKLSGSIS 179
    120 YVLGVPKMRERPIGDLVVGKLGADVDFLGTDCPPRVKVGIGLPGSKVYKLSGSIS 179
DB  120
OY  181 QYLSALLMAAPLALGDVEIEIIDLKLSIPYVEMTLRLMERFGVKAHSDSWDRFYIKGQ 240
    180 QYLSALLMAAPLALGDVEIEIIDLKLSIPYVEMTLRLMERFGVKAHSDSWDRFYIKGQ 239
DB  180
OY  241 KYKSPKNAAYVEGASASASYFLAGAAITGCTVTEGGCTTSLQGDVFAEVLLEMMGAKVTM 300
    240 KYKSPKNAAYVEGASASASYFLAGAAITGCTVTEGGCTTSLQGDVFAEVLLEMMGAKVTM 299
DB  240
OY  301 TETSIVTVTGQRPBPFGKRLKALIDVNMNKKAPDVAAVTLAAVVALPADPPTAIRDVAASRVK 360
    300 TETSIVTVTGQRPBPFGKRLKALIDVNMNKKAPDVAAVTLAAVVALPADPPTAIRDVAASRVK 359
DB  300
OY  361 TERMAVIRTELTLGASVEEGLDYCIITPEKLNVTAITDYDDHRMAMAFSLAACADVAV 420
    361 TERMAVIRTELTLGASVEEGLDYCIITPEKLNVTAITDYDDHRMAMAFSLAACADVAV 420

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DB  360 TERMAVIRTELTLGASVEEGDYCITVPEKLNVTAITDYDDHRMAMAFSLAACADVAV 419
OY  421 TIRDPGCTRKTRTPDPYFDVLSTFVK 445
    420 TIRDPGCTRKTRTPDPYFDVLSTFVK 444
DB  420

RESULT 15
ADQ37121
ID  ADQ37121 standard; protein; 511 AA.
XX
XX  ADQ37121;
XX
XX  AC
XX  ADQ37121;
XX
XX  DT  07-OCT-2004 (first entry)
XX
XX  DE  Cell proliferation-related polypeptide #126.
XX
XX  KW  cell proliferation related polypeptide; cell proliferation; senescence;
XX  differentiation; stress response.
XX
XX  OS  Oryza sativa.
XX
XX  PN  WO2004061122-A2.
XX
XX  PD  22-JUL-2004.
XX
XX  PF  23-DEC-2003; 2003MO-US041200.
XX
XX  PR  26-DEC-2002; 2002US-0436565P.
XX
XX  PA  (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX
XX  PI  Cooper B;
XX
XX  DR  WPI; 2004-53438/51.
XX
XX  PT  New nucleic acid molecule encoding a cell proliferation-related
XX  polypeptide, useful for modulating cell proliferation, senescence,
XX  differentiation, development, and stress response in plants, and for
XX  producing enhanced food crops.
XX
XX  PS  Disclosure; SEQ ID NO 280; 408bp; English.
XX
XX  CC  The present invention relates to an isolated nucleic acid molecule
XX  encoding a cell proliferation-related polypeptide. The nucleic acid
XX  molecule and the encoded polypeptide, and methods are useful for
XX  modulating cell proliferation, senescence, differentiation, development,
XX  and stress response in plants, and for producing enhanced food crops. The
XX  present sequence represents a cell proliferation-related polypeptide. The
XX  specification as EPO data.
XX
SQ  Sequence 511 AA;

Query Match          96.0%; Score 2165; DB 8; Length 511;
Best Local Similarity 95.1%; Pred. No. 4.2e-185;
Matches 423; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

OY  1 AGAEEVVLQPIKEISGVVKKLPGSKSLSNRIILLSALAEGLTVVDNLNSDVHYMLGALK 60
    67 AKAEEIVLQPIKEISGAVALPGSKSLSNRIILLSALAEGLTVVDNLNSDVHYMLGALK 126
DB  67
OY  61 TLGLSVBADKAAKRAVWVGCGGKFPVE-DAKEEVQLFLNAGTAMRSLTAATTAAGNAT 120
    127 ALGLSVBADKAAKRAVWVGCGGKFPVE-DAKEEVQLFLNAGTAMRPLTAATTAAGNAT 186
DB  127
OY  121 YVLGVPKMRERPIGDLVVGKLGADVDFLGTDCPPRVKVGIGLPGSKVYKLSGSIS 180
    187 YVLGVPKMRERPIGDLVVGKLGADVDFLGTDCPPRVKVGIGLPGSKVYKLSGSIS 246
DB  187
OY  181 QYLSALLMAAPLALGDVEIEIIDLKLSIPYVEMTLRLMERFGVKAHSDSWDRFYIKGQ 240
    181 QYLSALLMAAPLALGDVEIEIIDLKLSIPYVEMTLRLMERFGVKAHSDSWDRFYIKGQ 240

```

```

Db      247 QYLSALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSDRPIYKGGQ 306
Qy      241 KYSPKNAAYYBGSASSYFLAGAAITGCTVTVBEGCCTISLQGDVYKPAEYLEMNGAKVTW 300
Db      307 KYSPGNAAYVEGDASSASYFLAGAAITGCTVTVQCGCTISLQGDVYKPAEYLEMNGAKVTW 366
Qy      301 TETSVTVTGPOREPFGKHLKAIIDVNNNNKMPDVAMTLAVVALPADGPTAIRDVASNRVKE 360
Db      367 TDTSVTVTGPPREBYGKHLKAVDNNNNKMPDVAMTLAVVALPADGPTAIRDVASNRVKE 426
Qy      361 TERWVAIRTELTKLGASVEBGLDYCIITPEKLNVTALIDTYDDHRMAMAFSLAACADVPV 420
Db      427 TERWVAIRTELTKLGASVEBGLDYCIITPEKLNVTALIDTYDDHRMAMAFSLAACADVPV 486
Qy      421 TIRDPGCTRKTFFPDYFVNSTPYKN 445
Db      487 TIRDPGCTRKTFFPDYFVNSTPYKN 511

```

Search completed: September 15, 2005, 14:13:07
 Job time : 175 secs

1996-1997

GenCore version 5.1.6
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CM protein - protein search, using sw model

Run on: September 15, 2005, 13:57:16 ; Search time 179 Seconds

(Without alignments)
1273.046 Million cell updates/sec

Title: US-10-803-156-7

Perfect score: 2256

Sequence: 1 AGAEVVLQPIKISGVKL.....GCTRKTPPDVLTSPVKN 445

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing filter 45 summaries

Database: UniProt 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2256	100.0	445	2 095AK1	095AK1 eleusine in
2	2244	99.5	445	2 095AK0	095AK0 eleusine in
3	2199.5	97.5	444	2 024566	024566 zea mays (m
4	2165	96.0	511	2 093VK6	093VK6 oryza sativ
5	1962	87.0	519	2 06BE61	06BE61 conyza cana
6	1949.5	86.4	516	2 0946V0	0946V0 dicliptera
7	1943.5	86.1	516	2 0946U9	0946U9 dicliptera
8	1931	85.6	523	2 06BE64	06BE64 conyza cana
9	1929	85.5	391	2 080428	080428 conyza sativ
10	1927	85.4	516	1 AROA_PENTH	P11043 petunia hyb
11	1911	84.7	516	1 AROA_BRANA	P17688 brassica na
12	1909	84.6	518	2 08WIM5	08WIM5 cryophorag
13	1897	84.1	521	2 09PVP6	09PVP6 arabidopsis
14	1896	84.0	514	2 06UDV0	06UDV0 brassica ca
15	1896	84.0	518	1 ARO1_TOBAC	06JD40 nicotiana t
16	1893	83.9	521	2 08LC97	08LC97 arabidopsis
17	1888	83.7	520	1 AROA_ARATH	P05466 arabidopsis
18	1879	83.3	454	1 AROA_LYCES	06BE63 conyza cana
19	1877	83.2	530	1 AROA_LYCES	P10748 lycopersico
20	1664	73.8	347	2 09AT37	09AT37 lolium rigi
21	1597	70.8	358	2 06BE62	06BE62 erigeron an
22	1576	69.9	350	2 06BE61	06BE61 erigeron an
23	1545	68.5	357	2 06BE64	06BE64 amarantus
24	1490	66.0	338	1 ARO2_TOBAC	P23281 nicotiana t
25	1479.5	65.6	330	2 06VH15	06VH15 vitis vinif
26	1459	64.7	331	2 06VH44	06VH44 oryza sativ
27	1149	50.9	264	2 06BE60	06BE60 helianthus
28	1147	50.8	265	2 06BE66	06BE66 plantago la
29	1146	50.8	265	2 06BE68	06BE68 sarcocolla
30	1128	50.0	264	2 06BE69	06BE69 helianthus
31	1120.5	49.7	428	2 06EC18	06EC18 yerstinia ps

ALIGNMENTS

32	1119	49.6	428	2 06LPE1	06LPE1 photobacter
33	1118.5	49.6	428	1 AROA_YERPE	060112 yerstinia ps
34	1116	49.5	426	1 AROA_VIBCH	09KIB0 vibrio chol
35	1115	49.4	426	1 AROA_VIBPA	087QX9 vibrio para
36	1113.5	49.4	427	1 AROA_KLEPN	P24497 klebsiella
37	1113	49.3	428	2 07WJ45	07WJ45 vibrio vuln
38	1113	49.3	456	2 07NTR6	07NTR6 chromobacte
39	1109.5	49.2	427	1 AROA_ECOLI	P07638 escherichia
40	1108	49.1	427	1 AROA_YEREN	P19688 yerstinia en
41	1107.5	49.1	427	1 AROA_SHISO	09ZIF7 shigella so
42	1107.5	49.1	427	2 083RY8	083RY8 shigella fl
43	1104.5	49.0	428	2 07NED5	07NED5 photorhabd
44	1103.5	48.9	427	1 AROA_ECOL6	08JIB6 escherichia
45	1102.5	48.9	427	1 AROA_SHIDY	087006 shigella dy

RESULT 1

095AK1 PRELIMINARY; PRT; 445 AA.

ID 095AK1; 08H1B0;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE 5-enolpyruvylshikimate-3-phosphate synthase (EC 2.5.1.19)

DE (Fragment).

GN Name=epsps-R;

OS Eleusine indica (Goosegrass).

OC Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC PCCAD clade; Chloridoideae; Eragrostidae; Eleusine.

OX NCBI_Taxid=29674;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=22111148; PubMed=12114580; DOI=10.1104/pp.001560;

RA Baerson S.R., Rodriguez D.J., Tran M., Feng Y., Biebt N.A., Dill G.M.;

RT "Glucosyltransferase-resistant goosegrass. Identification of a mutation in the

target enzyme 5-enolpyruvylshikimate-3-phosphate synthase.";

RL Plant Physiol. 129:1265-1275(2002).

CC [2]

CC SEQUENCE FROM N.A.

RA Ng C.H., Wickneswari R., Salmijah S., Teng Y.T., Ismail B.S.;

RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.

CC -1- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate =

phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.

CC -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;

CC Sixth step.

CC -1- SIMILARITY: Belongs to the EPSP synthase family.

CC EMBL: AJ417033; CAD01095.1; -.

DR EMBL: AY157643; AAN63156.1; -.

DR HSSP: P07638; 1G6S.

DR GO: GO:0003866; P-3-phosphoshikimate 1-carboxyvinyltransferase. . .; IEA.

DR GO: GO:0016740; P:transferase activity; IEA.

DR GO: GO:0016089; P:aromatic amino acid family biosynthesis, sh. . .; IEA.

DR InterPro: IPR006264; AroA Ctrnsf.

DR InterPro: IPR001986; EPSP_synth.

DR Pfam: PF00275; EPSP_synthase; 1.

DR ProDom: PD001867; EPSP_synth; 1.

DR TrRfam: TRF01356; aroA; 1.

DR PROSITE: PS00104; EPSP_SYNTHASE_1; 1.

DR PROSITE: PS00885; EPSP_SYNTHASE_2; 1.

KW Amino-acid biosynthesis; Aromatic amino acid biosynthesis;

FT Transferase. 1

FT NON_TER 1

SQ SEQUENCE 445 AA; 47403 MW; CACC9BF4632D152F CRC64;

Query Match 100.0%; Score 2256; DB 2; Length 445;

Best Local Similarity 100.0%; Pred. No. 9,7e-147;

Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	AGAEVVLQJIKELSGVVLPGSKSLSNKILLSLALAGTVMNLIANSDEVHMLGALK	60
Dd	1 AGAEVVLQJIKELSGVVLPGSKSLSNKILLSLALAGTVMNLIANSDEVHMLGALK	60
Qy	61 TLGLSVADRAKRAVAVVGGCGKFPVEKDAKEEVLFLGNAGTANRSLTAAVTAAGNAT	120
Dd	61 TLGLSVADRAKRAVAVVGGCGKFPVEKDAKEEVLFLGNAGTANRSLTAAVTAAGNAT	120
Qy	121 YVLIDGVRMERPIGLVYVGLKQLGADVDCPLGTDCPPRAKYGGLPGGVKLSGSISS	180
Dd	121 YVLIDGVRMERPIGLVYVGLKQLGADVDCPLGTDCPPRAKYGGLPGGVKLSGSISS	180
Qy	181 QYLSALLMAAPLALGDAVEIILDKLISIPYEMTLRLMERFGVKAHSDSDMREYIKGGQ	240
Dd	181 QYLSALLMAAPLALGDAVEIILDKLISIPYEMTLRLMERFGVKAHSDSDMREYIKGGQ	240
Qy	241 KYSPKPAVYVEGDASASVFLAGAAITGGTIVTEGCGTTSLOGDVKEFAEVLMMGAVTM	300
Dd	241 KYSPKPAVYVEGDASASVFLAGAAITGGTIVTEGCGTTSLOGDVKEFAEVLMMGAVTM	300
Qy	301 TETSVMVTGSPORBPFGKHLKALIDVNMNMCPVANTLLVALLFADGPAITDVA\$MRYKE	360
Dd	301 TETSVMVTGSPORBPFGKHLKALIDVNMNMCPVANTLLVALLFADGPAITDVA\$MRYKE	360
Qy	361 TERWVAIRTELTKLGASVEBGLDYCIITPEBKLYNTAIDTYDDHRMAVAFSLAACADVPV	420
Dd	361 TERWVAIRTELTKLGASVEBGLDYCIITPEBKLYNTAIDTYDDHRMAVAFSLAACADVPV	420
Qy	421 TIRDPGCTRKTCPDPYEDULSTPKN	445
Dd	421 TIRDPGCTRKTCPDPYEDULSTPKN	445

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RESULT 2
Q95AKO PRELIMINARY; PRT; 445 AA.
AC Q95AKO; Q8HLB1;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE 5-enolpyruvylshikimate-2,3-phosphate synthase (EC 2.5.1.19)
DE (Fragment).
DE Name=epsps-S;
GN Eleusine indica (Goosegrass) .
OS Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Chloridoideae; Eragrostidae; Eleusine.
OX NCHI_TaxID=29674;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22111148; PubMed=12114580; DOI=10.1104/tp.001560;
RA Baerson S.R., Rodriguez D.J., Trem M., Feng Y., Bleet N.A., Dill G.M.;
RT "Glyphosate-resistant goosegrass: identification of a mutation in the
RT target enzyme 5-enolpyruvylshikimate-3-phosphate synthase.";
RL Plant Physiol. 129:1265-1275(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Ng C.H., Wichenawari R., Salimjah S., Teng Y.T., Imanil B.S.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate =
CC phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.
CC -1- PATHWAY: Aromatic amino acid biosynthesis; shikimate pathway;
CC sixth step.
CC -1- SIMILARITY: Belongs to the EPSP synthase family.
DR EMBL; AJ417034; CADD1096.1; -.
DR EMBL; AY157642; AAN63155.1; -.
DR HSSP; P07638; 1G6S.
DR GO; GO:0003986; F:3-phosphoshikimate 1-carboxyvinyltransferase . . ; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR006264; AroA_Ctransf.
DR InterPro; IPR001986; EPSP synth.

```

DR pfam: PF00275; BSP synthase; 1.
DR Prodom: PD001867; BSP synth; 1.
DR TIGRfams: TIGR01356; atcA; 1.
DR PROSITE: PS00104; BSP SYNTHASE_1; 1.
DR PROSITE: PS00885; BSP SYNTHASE_2; 1.
KW Amino-acid biosynthesis; Aromatic amino acid biosynthesis;
KW transylasease; 1
KW NON_TER 1
FT Q
SEQUENCE 445 AA; 47397 MW; 1878375C0925440 CRC64;

Query Match	99.5%	Score 2244	DB 2	Length 445
Best Local Similarity	99.6%	Pred. No. 6.5e-146		
Matches 443; Conservative	0	Mismatches 2	Indels 0	Gaps 0

Qy	1	AGAEVYLQPIKEISGVKJPGSSLSNRILLSLAGTIVVDLNLSEVDHYMLGALK	60
Db	1	AGAEVYLQPIKEISGVKJPGSSLSNRILLSLAGTIVVDLNLSEVDHYMLGALK	60
Qy	61	TLGSLVEADKAKRAVYVCGGKFPVEKDAAKEVOLFLGNAGTAMRSITAAVTAAGNAT	120
Db	61	TLGSLVEADKAKRAVYVCGGKFPVEKDAAKEVOLFLGNAGTAMRSITAAVTAAGNAT	120
Qy	121	YVLDGVPMMRRRPIGDLVYGLKQJGADVDCFLGTDCPVRVYKGIQGLPGGKYLSGSISS	180
Db	121	YVLDGVPMMRRRPIGDLVYGLKQJGADVDCFLGTDCPVRVYKGIQGLPGGKYLSGSISS	180
Qy	181	QYLSALMAAPLADGVIEIITDLKISIPYEYMTLRLMERPGVKAHSDSMRPFYIKGQ	240
Db	181	QYLSALMAAPLADGVIEIITDLKISIPYEYMTLRLMERPGVKAHSDSMRPFYIKGQ	240
Qy	241	KYKSPKNAVYEGDASSASYPLAGAAITGGITVBECCGTTSLQGDYKFAEVLMMGAKVTM	300
Db	241	KYKSPKNAVYEGDASSASYPLAGAAITGGITVBECCGTTSLQGDYKFAEVLMMGAKVTM	300
Qy	301	TEISVYVTGPORBPFGRRHLKALIDVNNKMPDVAMTTLAVALPADGPTAIRDVASMRVKE	360
Db	301	TEISVYVTGPORBPFGRRHLKALIDVNNKMPDVAMTTLAVALPADGPTAIRDVASMRVKE	360
Qy	361	TERVVALRTTELTKGASVEGLDVCITTPRKLNTALIDTYDDHDMAMAFSLAACADVAV	420
Db	361	TERVVALRTTELTKGASVEGLDVCITTPRKLNTALIDTYDDHDMAMAFSLAACADVAV	420

RESULT 3			
024566			
ID	024566	PRELIMINARY;	PRT; 444 AA.
AC	024566;		
DT	01-JAN-1998 (TREMBLrel. 05, Created)		
DT	01-JAN-1998 (TREMBLrel. 05, Last sequence update)		
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)		
DE	3-phosphoshikimate 1-carboxyvinyltransferase (psp-synthase) (BC 2.5.1.19) (Fragment).		
GN	Name=psp-s;		
OS	Zea mays (Maize).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;		
OC	Poaceae; Panicoidae; Andropogoneae; Zea.		
OX	NCBI_Taxid=4577;		
RM	[1]		
RP	SEQUENCE FROM N.A.		
RA	STRAIN=BMS;		
RC	Lebrun M., Freyssinet M., Sailland A., Rolland A., Freyssinet G.;		
RL	Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.		
RM	[2]		
RP	SEQUENCE FROM N.A.		
RA	STRAIN=BMS;		
RC	Lebrun M.C.;		
RL	Submitted (NOV-1991) to the EMBL/GenBank/DBJ databases.		
CC	-1- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate =		

CC phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.
 CC -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
 CC sixth step.
 CC -1- SIMILARITY: Belongs to the EPSP synthase family.
 DR HSPB; P07638; IM14.
 DR GO; GO:0003666; F:3-phosphoshikimate 1-carboxyvinyltransferase. . . ; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0016089; P:aromatic amino acid family biosynthesis, sh. . . ; IEA.
 DR InterPro; IPR006264; AroA_Ctransf.
 DR InterPro; IPR001986; EPSP_synth.
 DR Pfam; PF00275; EPSP synthase; 1.
 DR Prodom; PD001867; EPSP synth; 1.
 DR TIGRPFAM; TIGR01356; aroA_1.
 DR PROSITE; PS00104; EPSP SYNTHASE_1; 1.
 DR PROSITE; PS00885; EPSP SYNTHASE_2; 1.
 KW Amino-acid biosynthesis; Aromatic amino acid biosynthesis;
 KW transferase.
 FT NON TER 1 1
 SO SEQUENCE 444 AA; 47282 MW; 30EF0633CC671008 CRC64;
 Query Match 97.5%; Score 2199.5; DB 2; Length 444;
 Best Local Similarity 97.5%; Pred. No. 7,4e-143;
 Matches 434; Conservative 5; Mismatches 5; Indels 1; Gaps 1;
 QY 1 AGAEEVTLQPIKEISGVNKLPGSKSLSNRIILLSALAEQTVVDNLNSEDVHYMLGALK 60
 DB 1 AGAEEVTLQPIKEISGVNKLPGSKSLSNRIILLSALAEQTVVDNLNSEDVHYMLGALK 60
 QY 61 TLGLSVEADKAKRAVAVVGGCGKFPVEKDKEEVQLFLGNAGTANRSLTAAVTAAGNAT 120
 DB 61 TLGLSVEADKAKRAVAVVGGCGKFPVEKDKEEVQLFLGNAGTANRSLTAAVTAAGNAT 119
 QY 121 YVLGVPRMRERPIGDLVVGKQLGADVDFCLGTDCEPVRVKGIGLPGKVKLSGSIS 180
 DB 120 YVLGVPRMRERPIGDLVVGKQLGADVDFCLGTDCEPVRVKGIGLPGKVKLSGSIS 179
 QY 181 QYLSALLMAAPLALGDVEIEIIDKLSIPYEMTLRLMERFGVKAHSDSMDRFYIKGQ 240
 DB 180 QYLSALLMAAPLALGDVEIEIIDKLSIPYEMTLRLMERFGVKAHSDSMDRFYIKGQ 239
 QY 241 KYKSPKNAVVEGDASASVFLAGAITGTVVEGCGTTSLOGDVKFAVLEMMGAKVTM 300
 DB 240 KYKSPKNAVVEGDASASVFLAGAITGTVVEGCGTTSLOGDVKFAVLEMMGAKVTM 299
 QY 301 TETSVTVTGPOREPFGKRLKALDVNNKMPDVAMTLAVVAFADGPTAIRDVASRWYKE 360
 DB 300 TETSVTVTGPOREPFGKRLKALDVNNKMPDVAMTLAVVAFADGPTAIRDVASRWYKE 359
 QY 361 TERMAVAIRTELTKGASVEBGIDYCIITPEKLNATRIDYDDHMAAFSLAACADVPV 420
 DB 360 TERMAVAIRTELTKGASVEBGIDYCIITPEKLNATRIDYDDHMAAFSLAACADVPV 419
 QY 421 TIRDPGCTRKTFPDYFDVLSFTVKN 445
 DB 420 TIRDPGCTRKTFPDYFDVLSFTVKN 444

RESULT 4
 Q93VK6 PRELIMINARY; PRT; 511 AA.
 AC Q93VK6;
 DT 01-DEC-2001 (TEMBLrel. 19, Created)
 DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
 DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
 DE 3-phosphoshikimate 1-carboxyvinyltransferase (5-enolpyruvylshikimate
 3-phosphate synthase) (EPSP synthase).
 GN Name=EPSPS;
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 NCBI_TaxId=4530;
 OX

RN [1]
 RP SEQUENCE FROM N.A.
 RA Wu L., Nagano H., Yoshida K., Kawaesaki S., Kishima Y., Sano Y.;
 RL Submitted (DEC-2000) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Wang X.J., Jiang F.D., Gang L.X., Zhen Z.;
 RT Isolation and characterization of rice EPSP synthase and its
 RT chromosome location.
 RL Sci. Sin., Ser. B, Chem. Biol. Agric. Med. Earth Sci. 0:0-0(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Wang X.J., Zhen Z.;
 RL Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate =
 CC phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.
 CC -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
 CC sixth step.
 CC -1- SIMILARITY: Belongs to the EPSP synthase family.
 DR EMBL; AB052962; BAB61062.1; -.
 DR EMBL; AF413081; AAL06593.1; -.
 DR EMBL; AF413082; AAL07437.1; -.
 DR HSPB; P07638; 1G6S.
 DR Gramene; Q93VK6; -.
 DR GO; GO:0003666; F:3-phosphoshikimate 1-carboxyvinyltransferase. . . ; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0016089; P:aromatic amino acid family biosynthesis, sh. . . ; IEA.
 DR InterPro; IPR006264; AroA_Ctransf.
 DR InterPro; IPR001986; EPSP_synth.
 DR Pfam; PF00275; EPSP synthase; 1.
 DR Prodom; PD001867; EPSP synth; 1.
 DR TIGRPFAM; TIGR01356; aroA_1.
 DR PROSITE; PS00104; EPSP SYNTHASE_1; 1.
 DR PROSITE; PS00885; EPSP SYNTHASE_2; 1.
 KW Amino-acid biosynthesis; Aromatic amino acid biosynthesis;
 KW transferase.
 SO SEQUENCE 511 AA; 53971 MW; A4265CB513C840AB CRC64;
 Query Match 96.0%; Score 2165; DB 2; Length 511;
 Best Local Similarity 95.1%; Pred. No. 2e-140;
 Matches 423; Conservative 13; Mismatches 9; Indels 0; Gaps 0;
 QY 1 AGAEEVTLQPIKEISGVNKLPGSKSLSNRIILLSALAEQTVVDNLNSEDVHYMLGALK 60
 DB 67 AGAEEVTLQPIKEISGVNKLPGSKSLSNRIILLSALAEQTVVDNLNSEDVHYMLGALK 126
 QY 61 TLGLSVEADKAKRAVAVVGGCGKFPVEKDKEEVQLFLGNAGTANRSLTAAVTAAGNAT 120
 DB 127 ALGLSVEADKAKRAVAVVGGCGKFPVEKDKEEVQLFLGNAGTANRSLTAAVTAAGNAT 186
 QY 121 YVLGVPRMRERPIGDLVVGKQLGADVDFCLGTDCEPVRVKGIGLPGKVKLSGSIS 180
 DB 187 YVLGVPRMRERPIGDLVVGKQLGADVDFCLGTDCEPVRVKGIGLPGKVKLSGSIS 246
 QY 181 QYLSALLMAAPLALGDVEIEIIDKLSIPYEMTLRLMERFGVKAHSDSMDRFYIKGQ 240
 DB 247 QYLSALLMAAPLALGDVEIEIIDKLSIPYEMTLRLMERFGVKAHSDSMDRFYIKGQ 306
 QY 241 KYKSPKNAVVEGDASASVFLAGAITGTVVEGCGTTSLOGDVKFAVLEMMGAKVTM 300
 DB 307 KYKSPKNAVVEGDASASVFLAGAITGTVVEGCGTTSLOGDVKFAVLEMMGAKVTM 366
 QY 301 TETSVTVTGPOREPFGKRLKALDVNNKMPDVAMTLAVVAFADGPTAIRDVASRWYKE 360
 DB 367 TETSVTVTGPOREPFGKRLKALDVNNKMPDVAMTLAVVAFADGPTAIRDVASRWYKE 426
 QY 361 TERMAVAIRTELTKGASVEBGIDYCIITPEKLNATRIDYDDHMAAFSLAACADVPV 420
 DB 427 TERMAVAIRTELTKGASVEBGIDYCIITPEKLNATRIDYDDHMAAFSLAACADVPV 486
 QY 421 TIRDPGCTRKTFPDYFDVLSFTVKN 445
 DB 487 TIRDPGCTRKTFPDYFDVLSFTVKN 511


```

RESULT 5
ID Q6E6L5 PRELIMINARY, PRT, 519 AA.
AC Q6E6L5;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE 5-enol-pyruvylshikimate-phosphate synthase.
GN Name=EPSPS1.
OS Conyza canadensis.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Campanulidae; Asterales; Asteraceae; Asteroideae; Asteraceae; Conyza.
OX NCBI_TaxId=12917;
RN [1]
RP SEQUENCE FROM N.A.
RA Heck G.R., Alibhai M., Hubmeier C.S., Flaesink S., Malven M., Qi Y.,
RA Chen Y.-C.S., Bunkers G.J., Sammons R.D., Feng P.C.C., Foadey W.T.,
RA Jacob C.A.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate =
CC phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.
CC -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
CC sixth step.
CC -1- SIMILARITY: Belongs to the EPSP synthase family.
DR EMBL: AY545666; AF745243.1; -;
DR GO: GO:0003866; F:3-phosphoshikimate 1-carboxyvinyltransferase. . .; IEA.
DR GO: GO:0016089; P:aromatic amino acid family biosynthesis. sh. . .; IEA.
DR InterPro: IPR006264; ArcoA.Ctransf.
DR InterPro: IPR001986; EPSP synth.
DR Pfam: PF00275; EPSP synthase; 1.
DR Prodom: PD001867; EPSP synth; 1.
DR TIGRfam: TIGR01356; aroA. 1.
DR PROSITE: PS00104; EPSP SYNTHASE_1; 1.
DR PROSITE: PS00885; EPSP SYNTHASE_2; 1.
DR Amino-acid biosynthesis; Aromatic amino acid biosynthesis;
DR Transferrase.
KW SEQUENCE 519 AA; 55210 MW; 47F6706C8CDBE3 CRC64;
SQ
Query Match 87.0%; Score 1962; DB 2; Length 519;
Best Local Similarity 85.5%; Pred. No. 1.8e-126;
Matches 377; Conservative 34; Mismatches 30; Indels 0; Gaps 0;
QY 5 EYVLQPIKEISGVVYKPGSKSLSNRIILLSALAEGLTVVNDNLNSBDVHYMLGALTKTGL 64
DB 79 EYVLQPIKEISGVVYKPGSKSLSNRIILLSALAEGLTVVNDNLNSBDVHYMLGALTKTGL 138
QY 65 SYEADKAARAVVVGCGKFPVEKDAKEVOLFLNAGTAMRSLTAATVAAGNATYYLD 124
DB 139 NVEEDVAIKRAIVGGCGVFPVGEKAKDQFLNAGTAMRPLTAATVAAGNATYYLD 198
QY 125 GYPRMRERPIGDLVGLKQLGADVDCFLGTCPPRVKIGLPGKVKLSGSSISQYIS 184
DB 199 GYPRMRERPIGDLVGLKQLGADVDCFLGTCPPRVKIGLPGKVKLSGSSISQYIS 258
QY 185 ALMAAPALAGDVEIEIIDLKISIPYEMTLRLMERPGVKAHSDMDRFFYIKGGOKYKS 244
DB 259 ALMAAPALAGDVEIEIIDLKISIPYEMTLRLMERPGVKAHSDMDRFFYIKGGOKYKS 318
QY 245 PKNAAYVEGDASASAYFLAGAAITGGTVVVEGCGTSLQGDVFAEVLGMAKAVTWETS 304
DB 319 PKNAAYVEGDASASAYFLAGAAITGGTVVVEGCGTSLQGDVFAEVLGMAKAVTWETS 378
QY 305 VVTYTGPOREPFGRKRLKALIDVNMNMKPDVAMTLAAVALPADGPTAIRDVASRWKETERM 364
DB 379 VVTYTGPOREPFGRKRLKALIDVNMNMKPDVAMTLAAVALPADGPTAIRDVASRWKETERM 438
QY 365 VALRTETLTKGASVEGLDYCIITPPEKLVNTAIDYDDHRMAMASIAACADVPTIID 424
DB 439 IALCTELRKLGAIVBEGPDYCVIITPPEKLVNTAIDYDDHRMAMASIAACADVPTIID 498

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QY 425 PGCTRTPEPDYEDVLSTFVKN 445
DB 499 PGCTRTPEPDYEDVLSTFVKN 519
RESULT 6
ID Q946V0 PRELIMINARY, PRT, 516 AA.
AC Q946V0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 5-enolpyruvylshikimate-3-phosphate synthase.
OS Dicotyledonaceae.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Lamiales; Acanthaceae; Acanthoideae; Ruellieae; Duetichneae;
OC Dicotyledonaceae.
OX NCBI_TaxId=173162;
RN [1]
RP SEQUENCE FROM N.A.
RA Yuan C.I., Chiang M.Y., Chen Y.M.;
RT "Triple mechanisms of glyphosate-resistance in a naturally occurring
RT glyphosate-resistant plant Dicotyledonaceae."
RL Plant Sci. 163:543-554(2002).
CC -1- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate =
CC phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.
CC -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
CC sixth step.
CC -1- SIMILARITY: Belongs to the EPSP synthase family.
DR EMBL: AF371965; AAL27697.1; -;
DR HSSP: P07638; 1G6S.
DR GO: GO:0003866; F:3-phosphoshikimate 1-carboxyvinyltransferase. . .; IEA.
DR GO: GO:0016740; F:transferase activity; IEA.
DR GO: GO:0016089; P:aromatic amino acid family biosynthesis. sh. . .; IEA.
DR InterPro: IPR006264; ArcoA.Ctransf.
DR InterPro: IPR001986; EPSP synth.
DR Pfam: PF00275; EPSP synthase; 1.
DR Prodom: PD001867; EPSP synth; 1.
DR TIGRfam: TIGR01356; aroA. 1.
DR PROSITE: PS00104; EPSP SYNTHASE_1; 1.
DR PROSITE: PS00885; EPSP SYNTHASE_2; 1.
DR Amino-acid biosynthesis; Aromatic amino acid biosynthesis;
DR Transferrase.
KW SEQUENCE 516 AA; 54913 MW; B8C1396F0F1D2D18 CRC64;
SQ
Query Match 86.4%; Score 1949.5; DB 2; Length 516;
Best Local Similarity 85.6%; Pred. No. 1.3e-125;
Matches 375; Conservative 37; Mismatches 25; Indels 1; Gaps 1;
QY 5 EYVLQPIKEISGVVYKPGSKSLSNRIILLSALAEGLTVVNDNLNSBDVHYMLGALTKTGL 64
DB 77 EYVLQPIKEISGVVYKPGSKSLSNRIILLSALAEGLTVVNDNLNSBDVHYMLGALTKTGL 136
QY 65 SYEADKAARAVVVGCGKFPVEKDAKEVOLFLNAGTAMRSLTAATVAAGNATYYLD 124
DB 137 AVEEDKAKNAKAVVEGCGVFPVGEKAKDQFLNAGTAMRPLTAATVAAGNATYYLD 196
QY 125 GYPRMRERPIGDLVGLKQLGADVDCFLGTCPPRVKIGLPGKVKLSGSSISQYIS 184
DB 197 GYPRMRERPIGDLVGLKQLGADVDCFLGTCPPRVKIGLPGKVKLSGSSISQYIS 256
QY 185 ALMAAPALAGDVEIEIIDLKISIPYEMTLRLMERPGVKAHSDMDRFFYIKGGOKYKS 244
DB 257 ALMAAPALAGDVEIEIIDLKISIPYEMTLRLMERPGVKAHSDMDRFFYIKGGOKYKS 316
QY 245 PKNAAYVEGDASASAYFLAGAAITGGTVVVEGCGTSLQGDVFAEVLGMAKAVTWETS 304
DB 317 PKNAAYVEGDASASAYFLAGAAITGGTVVVEGCGTSLQGDVFAEVLGMAKAVTWETS 376
QY 305 VVTYTGPOREPFGRKRLKALIDVNMNMKPDVAMTLAAVALPADGPTAIRDVASRWKETERM 364
DB 377 VVTYTGPOREPFGRKRLKALIDVNMNMKPDVAMTLAAVALPADGPTAIRDVASRWKETERM 435

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QY	365	VAIRRELTGASVVEGDDYCIITTPREKNTAIDTYDDHRMAAFSLAACADVPYITD	424
DB	436	IAICETLRDGAIVVEGDPDYCIITPEKNTAIDTYDDHRMAAFSLAACADVPYITD	495
QY	425	PGCTRKTPPDYFDVLTSTF 442	
DB	496	PGCTRKTPPDYFDVLTSTY 513	
RESULT 7			
ID	0946U9	PRELIMINARY; PRT; 516 AA.	
AC	0946U9;		
DT	01-DEC-2001 (TREMBLrel. 19, Created)		
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)		
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)		
DE	5-enolpyruvylshikimate-3-phosphate synthase B.		
OS	Dicliptera chinensis.		
OC	Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons: core eudicots; asterids;		
OC	lamiales; Lamiales; Acanthaceae; Acanthoideae; Ruellieae; Dufletieae;		
OC	Dicliptera.		
OX	NCBI_TaxId=173162;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Yuan C.T., Chiang M.Y., Chen Y.M.;		
RT	"Triple mechanisms of glyphosate-resistance in a naturally occurring		
RT	glyphosate-resistant plant <i>Dicliptera chinensis</i> ."		
RL	Plant Sci. 163:543-554(2002).		
CC	-1- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate =		
CC	3-phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.		
CC	-1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;		
CC	8th step.		
CC	-1- SIMILARITY: Belongs to the EPSP synthase family.		
DR	EMBL, AF371966; AL27698.1; --		
DR	HSSP, P07638; I668.		
DR	GO: GO:0003866; F:3-phosphoshikimate 1-carboxyvinyltransferase. . ; IEA.		
DR	GO: GO:0016740; P:transferase activity, IEA.		
DR	GO: GO:0016089; P:aromatic amino acid family biosynthesis, sh. . ; IEA.		
DR	InterPro, IPR006264; ArCA_Ctransf.		
DR	InterPro, IPR001986; EPSP_synth.		
DR	Pfam, PF00275; EPSP_synthase; 1.		
DR	Prodom, P0001867; EPSP_synth; 1.		
DR	TIGRFAMs, TIGR01356; atcA; 1.		
DR	PROSITE, PS00885; EPSP_SYNTHASE_2; 1.		
KW	Amino-acid biosynthesis; Aromatic amino acid biosynthesis;		
KW	transferase.		
SC	SEQUENCE 516 AA; 54997 MW; 680848DD5959B56 CRC64;		
Query Match 86.1%; Score 1943.5; DB 2; Length 516;			
Best Local Similarity 85.4%; Pred. No. 3,4e-125;			
Matches 374; Conservative 36; Mismatches 27; Indels 1; Gaps 1.			
QY	5	EVLVLPKIRISGVNVLPGSKSLSNRIILLSLAAEGTVDNLLNSEDVHYMLGALTKGL 64	
DB	77	EIVLQPIDISGTIVLPGSKSLSNRVLLLAALSEGTVVNNLSSEDDHYMLGALRTGL 136	
QY	65	SVEADKAARAVVVGCGGKFPVYKADKEVQLFLNAGTAMRSLTAAYTAAGNATVYLD 124	
DB	137	HYEEDKAKAVVEGCGQFPASKEGKDEIQLFLKAGTAMRPLTAAYTAAGNARVYLD 196	
QY	125	GVPRRRERPIGLVVGKQLGADVNCFLGCTDPPRVYKIGIGLPGKRYLSSSISQYLS 184	
DB	197	GVPRRRERPIGLVVGKQLGADVNCFLGCTDPPRVYKIGIGLPGKRYLSSSISQYLT 256	
QY	185	ALLMAAPALAGVEIEIIDKLISIPYEVNTILALMRFVKASHSDMPRTYKGGQYKS 244	
DB	257	ALLMSAPALAGVEIEIYDKLSIVYEVNTILALMRFVYVHTDMDRLIRGGQYKS 316	
QY	245	PKNAVVEGDASASVFLAGAAITGGTVYVEGCGTTSLOGDVFAVLEMMGAKVTYETS 304	
DB	317	PKNAVVEGDASASVFLAGAAITGGTVYVEGCGTTSLOGDVFAVLEMMGAKVNTENS 376	

Oy		305	VTVTSPQSPGPPGRKRLKALIDVNMATOMPVDVAAMTLAVVALPADCPTRAI RDVASNRVKETERN	364
Dd		377	VTVTPGPPEVP-P-GKKHRAIDVMNMPDPVAMTLAVVALPADPPTAIRDVASNRVKETERB	435
Oy		365	VAIRBELRKLGASVEEGLDYCIITPEPEKLNVTAIDTYDDHRMAMA.FSLAACADVPRTIRD	424
Dd		436	IATLTKLRKGVTAEGBPDYCIIITPEPEKLNVTAIDTYDDHRMAMFSLAACADVPTIKD	495
Oy		425	PCTRKTPEPDFVDLPSTP 442	
Dd		496	PGCTRKTPEPNFDVLSTY 513	
 RESULT 8 06E6I4				
ID	06E6I4	PRELIMINARY;	PRT;	523 AA.
AC	06E6I4			
DT	25-OCT-2004 (TREMBLrel. 28, Created)			
DT	25-OCT-2004 (TREMBLrel. 28, Last sequence update)			
DT	25-OCT-2004 (TREMBLrel. 28, Last annotation update)			
DE	5-enol-pyruvylshikimate-phosphate synthase.			
EN	Name=EPSPS2;			
OS	Conyza canadensis.			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;			
OC	campnellids; Asterales; Asteraceae; Asteroideae; Asteraceae; Conyza.			
OX	NCBI_TaxId=72917;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Heck G.R., Alibhai M., Huhmeier C.S., Plasinski S., Malven M., Qi Y.,			
RA	Chen Y.-C.S., Bunkers G.J., Sammons R.D., Feng P.C.C., Poadey W.T.,			
RA	Cadacoc C.A.;			
RL	Submitted (FEBS-2004) to the EMBL/GenBank/DDBJ databases.			
CC	-1- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate =			
CC	phosphate + 5-O-(l-carboxyviny)l-3-phosphoshikimate.			
CC	-1- PATHWAY: Aromatic amino acid biosynthesis; shikimate pathway;			
CC	sixth step.			
CC	-1- SIMILARITY: Belongs to the EPSP synthase family.			
DR	EMBL; AY545667; AAT45244.1; .			
DR	GO; GO:0003866; F:3-phosphoshikimate 1-carboxyvinyltransferas. . ; IEA.			
DR	GO; GO:0016089; P:aromatic amino acid family biosynthesis, sh. . ; IEA.			
DR	InterPro; IPR001986; ArCo_Ctransf.			
DR	InterPro; IPR001986; EPSP_synth.			
DR	Pfam; PF00275; EPSP_synthase; 1.			
DR	ProDom; PD001867; EPSP_synth; 1.			
DR	TIGRFAMS; TIGR01356; atoa; 1.			
DR	PROSITE; PS00104; EPSP SYNTHASE_1; 1.			
DR	PROSITE; PS00885; EPSP SYNTHASE_2; 1.			
KW	Amino-acid biosynthesiss; Aromatic amino acid biosynthesiss;			
KW	Transferrase.			
SC	SEQUENCE 523 AA; 55811 MW; 24B2799B042D95F6 CRC64;			
 Query Match 85.6%; Score 1931; DB 2; Length 523; Best Local Similarity 83.5%; Pred. No.2.5e-124; Matches 369; Conservative 40; Mismatches 33; Indels 0; Gaps 0				
Oy		4	EEVYLQPIKEISGVVKLPGRSKSLNSNRILLLSALAEGTTVVNDLINSDEVHTNLGALKTIYG 63	
Dd		82	EEIVLKPIQIISGTVHLPGRSKSLNSRRILLLAALSEGTTVVNDLINSDDVHYMLGALRALG 141	
Oy		64	LSVEDAKRAKAAVVGCGGCKPPEVEDADEBEVQLPLFGNGATMARSLTAANTAAAGNAITYL 123	
Dd		142	LNVENSNIKKAIVTEGGCGFPVPGKEADEIQLFPGNGATMRPLTAANTAAAGNASSYYL 201	
Oy		124	DGVPRMERPRIGDLVVGKLGADVDCTGLDPCPPRVKAGLIGLPGCKRYKLSGSISSQYL 183	
Dd		202	DGVPRMERPRIGDLVLTGKLGAGVDCSLGTCNPCEPVRVVSGGLPGCKRYKLSGSISSQYL 261	
Oy		184	SALLMAAPLALGDVIEIBIIDYLISIPYEVTLLRMERFGVKAHSDSMDRFYIKGGQQYK 243	
Dd		262	TSLMAAPLALGDVIEIIVDKLISIPYEVTMLKIMERGVAVEHSDTWDRFTVRGGQYK 321	

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QY 244 SPKNAYVEGDASASYFLAGAATGGTGTVEGGCTTSLGQDVFAEVLMMGAKWTMTET 303
DB 322 SPENAYVEGDASASYFLAGAATGGTGTVEGGCTTSLGQDVFAEVLMMGAKWTMTEN 381
QY 304 SVTVTGPQEPPEPFGKRLKALIDVNMNMKPDVAMTLAVVALPADGPTAIRDVA 363
DB 382 SVTVKPPRRSSGRGHLRPVDVNMNMKPDVAMTLAVVALYADGPTAIRDVA 441
QY 364 MVAIRTELTLGASVEEGLDYCIITPPEKLNVAITDTHRRAMA 423
DB 442 MINICTELKRLGATVEEGPDYCVITPPEKLNVAITDTHRRAMA 501
QY 424 DPCTRKTPEPDYFDVLTFTVKN 445
DB 502 DPCTRKTPEPDYFDVLTFTVKN 523

RESULT 9
ID 080428 PRELIMINARY; PRT; 391 AA.
AC 080428;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE 3-phosphoshikimate 1-carboxyvinyltransferase.
GN Name=epsp-8; Synonyms=P0679C08.29;
OS Oryza sativa (Japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriactoidae; Oryzaceae; Oryza.
OX NCBI_Taxid=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=T65wx;
RA Kishima Y., Sano Y.;
RL Submitted (Aug-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate =
CC phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.
CC -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
CC sixth step.
CC -1- SIMILARITY: Belongs to the EPSP synthase family.
DR EMBL; AB016765; BAA32376.1; -.
DR EMBL; AP002542; BAB19389.1; -.
DR HSSP; P07638; I66S.
DR Gramene; O80428; -.
DR GO; GO:0003866; F:3-phosphoshikimate 1-carboxyvinyltransferase. . .; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0016089; P:aromatic amino acid family biosynthesis, sh. . .; IEA.
DR InterPro; IPR006264; AroA_Ctransf.
DR InterPro; IPR001986; EPSP_synth.
DR Pfam; PF00275; EPSP_synthase; 1.
DR ProDom; PD001867; EPSP_synth. 1.
DR TIGRfam; TIGR01356; aroA; 1.
DR PROSITE; PS00104; EPSP_SYNTHASE_1; 1.
DR PROSITE; PS00885; EPSP_SYNTHASE_2; 1.
KW Amino-acid biosynthesis; Aromatic amino acid biosynthesis;
KW transferase.
SQ SEQUENCE 391 AA; 41709 MW; CB3FL7C39F30ACBD CRC64;

Query Match 85.5%; Score 1929; DB 2; Length 391;
Best Local Similarity 95.9%; Pred. No. 2.4e-124;
Matches 3/5; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 55 MGLALTLGLSVADRAAKAAVAVVGGGKPEVEKAEVQLFLGAGTAMSLTAAYTA 114
DB 1 MGLALTLGLSVADRAAKAAVAVVGGGKPEVEKAEVQLFLGAGTAMSLTAAYTA 60
QY 115 AGGNATYVLDGVRMRERPIGDLVVLKQLGADVDFLTGDCPPVVKIGIGLPGKVTL 174

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DB 61 AGGNATYVLDGVRMRERPIGDLVVLKQLGADVDFLTGDCPPVVKIGIGLPGKVTL 120
QY 175 SGISSOYLIALMAAPALGVEIETDKLISIPYEMTLKMRFGVKAHSDSMDF 234
DB 121 SGISSOYLIALMAAPALGVEIETDKLISIPYEMTLKMRFGVKAHSDSMDF 180
QY 235 YIKGQKPKSPKNAYVEGDASASYFLAGAATGGTGTVEGGCTTSLGQDVFAEVLMM 294
DB 181 YIKGQKPKSPKNAYVEGDASASYFLAGAATGGTGTVEGGCTTSLGQDVFAEVLMM 240
QY 295 GAKVTMTSTSTVTGPQEPPEPFGKRLKALIDVNMNMKPDVAMTLAVVALPADGPTAIRDVA 354
DB 241 GAKVTMTSTSTVTGPQEPPEPFGKRLKALIDVNMNMKPDVAMTLAVVALPADGPTAIRDVA 300
QY 355 SMRVKETERMVAIRTELTLGASVEEGLDYCIITPPEKLNVAITDTHRRAMA 414
DB 301 SMRVKETERMVAIRTELTLGASVEEGLDYCIITPPEKLNVAITDTHRRAMA 360
QY 415 CADVPVTIRDPCTRKTPEPDYFDVLTFTVKN 445
DB 361 CADVPVTIRDPCTRKTPEPDYFDVLTFTVKN 391

RESULT 10
ID AROA_PETHY STANDARD; PRT; 516 AA.
AC P11043;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 3-phosphoshikimate 1-carboxyvinyltransferase, chloroplast precursor
DE (EC 2.5.1.19) (5-enolpyruvylshikimate-3-phosphate synthase) (Epsp
DE synthase).
OS Petunia hybrida (Petunia).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Petunia.
OX NCBI_Taxid=4102;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Mitchell;
RX MEDLINE=88153749; PubMed=3346248;
RA Gasser C.S., Winter J.A., Hironaka C.M., Shah D.M.;
RT "Structure, expression, and evolution of the 5-enolpyruvylshikimate-3-
RT phosphate synthase gene of petunia and tomato.";
RL J. Biol. Chem. 263:4280-4289(1988).
RN [2]
RP MUTAGENESIS OF GLY-173.
RX MEDLINE=92042175; PubMed=1939260;
RA Padgett S.R., Re D.B., Gasser C.S., Eicholtz D.A., Frazier R.B.,
RA Hironaka C.M., Levine E.B., Shah D.M., Fraley R.T., Kishore G.M.;
RT "Site-directed mutagenesis of a conserved region of the 5-
RT enolpyruvylshikimate-3-phosphate synthase active site.";
RL J. Biol. Chem. 266:22364-22369(1991).
CC -1- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate =
CC phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.
CC -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
CC sixth step.
CC -1- SUBCELLULAR LOCATION: Chloroplast.
CC -1- MISCELLANEOUS: This enzyme is the target of the potent, broad-
CC spectrum herbicide, glyphosate [n-(phosphonomethyl)glycine].
CC Overproduction of EPSP leads to glyphosate tolerance.
CC -1- SIMILARITY: Belongs to the EPSP synthase family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC or send an email to license@isb.ch).
CC -----
CC EMBL; M21084; AAA33699.1; -.

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DR PIR; A26198; XUPJVS.
 DR HSSP; P07638; 1G6S; AROA.
 DR InterPro; IPR001986; EPSP_synth.
 DR Pfam; PF00275; EPSP_synthase; 1.
 DR ProDom; PD001867; EPSP_synth; 1.
 DR TIGRfam; TIGR01356; aroA; 1.
 DR PROSITE; PS00104; EPSP_SYNTHASE_1; 1.
 DR PROSITE; PS00885; EPSP_SYNTHASE_2; 1.
 DR Aromatic amino acid biosynthesis; Chloroplaest; Herbicide resistance;
 KM Transferrase; Transf. peptide.
 FT TRANSIT 1 72 Chloroplaest.
 FT CHAIN 73 516 carboxyvinyltransferrase.
 FT MUTAGEN 173 173 G-A: Resistance to glyphosate.
 SQ SEQUENCE 516 AA; 55537 MW; 1A753E717BE7BAF8 CRC64;
 Query Match 85.4%; Score 1927; DB 1; Length 516;
 Best Local Similarity 84.4%; Pred. No. 4,6e-124;
 Matches 372; Conservative 31; Mismatches 38; Indels 0; Gaps 0;
 QY 5 EVVLQPIKEISGVVKKLPGSKSLNSRIILLALSALAEFTTVNINLSSEVHYMLGALKTLGL 64
 DB 76 EIVLQPIKEISGVVKKLPGSKSLNSRIILLALSALAEFTTVNINLSSEVHYMLGALKTLGL 135
 QY 65 SVEADKAAKAAVAVVGGCGKFPVKKAKKEVQLFLGNAAGTMRSLTAATPAAGNATVVD 124
 DB 136 HVEEDSANQRAVVEGGCGLEFPVKESEKEEQLFLGNAAGTMRSLTAATPAAGNATVVD 195
 QY 125 GVPKMERPIGDLVVGKLGADVDGFLGDCPPVAVKIGLPGGKVLGSGISSQYLS 184
 DB 196 GVPKMERPIGDLVVGKLGADVDGFLGDCPPVAVKIGLPGGKVLGSGISSQYLS 255
 QY 185 ALIAPALAGDVEIEIIDLKISIPYEMTLRLMERFGVAEHSDSMDRPFYKGGQKYS 244
 DB 256 ALIAPALAGDVEIEIIDLKISIPYEMTLRLMERFGVAEHSDSMDRPFYKGGQKYS 315
 QY 245 PKAAVVEGDSASVFLAGAAITGGTVVVEGCGTTLQGDVKAETLEMMGAVTTTENS 304
 DB 316 PKAAVVEGDSASVFLAGAAITGGTVVVEGCGTTLQGDVKAETLEMMGAVTTTENS 375
 QY 305 VVTVGQRPFPGRKHLKAIDVNNKMPDVAMTLAVVALFADGPTAIRDVASMKVETERN 364
 DB 376 VVTVGQRPFPGRKHLKAIDVNNKMPDVAMTLAVVALFADGPTAIRDVASMKVETERN 435
 QY 365 VAIKTELTKLGASVEEGDLVCIITPPEKLVNTAIDTYDDHRMAAFSLAACADVPVTIR 424
 DB 436 VAIKTELTKLGASVEEGDLVCIITPPEKLVNTAIDTYDDHRMAAFSLAACADVPVTIR 495
 QY 425 PGCTRTKTFPPYFDVLSTFVN 445
 DB 496 PGCTRTKTFPPYFDVLSTFVN 516
 RESULT 11
 AROA_BRANA STANDARD; PRT; 516 AA.
 ID AROA_BRANA STANDARD; PRT; 516 AA.
 AC P17688;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 3-phosphoshikimate 1-carboxyvinyltransferrase, chloroplaest precursor
 DE (EC 2.5.1.19) (5-enolpyruvylshikimate-3-phosphate synthase) (EPSP
 synthase).
 OS Brassica napus (Rape).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC euroside II; Brassicales; Brassicaceae; Brassica.
 OK NCBI_TaxID=3708;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV, Weibull;
 RX MEDLINE=90251470; PubMed=2339069;

RA Gasser C.S., Klee H.J.;
 "A. Brassica napus gene encoding 5-enolpyruvylshikimate-3-phosphate
 synthase."
 RT Nucleic Acids Res. 18:2821-2821 (1990).
 RL Nucleic Acids Res. 18:2821-2821 (1990).
 CC -1- CARLYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate =
 CC phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.
 CC -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
 CC sixth step.
 CC -1- SUBCELLULAR LOCATION: Chloroplaest.
 CC -1- MISCELLANEOUS: This enzyme is the target of the potent, broad-
 CC spectrum herbicide, glyphosate [n-(phosphonomethyl)glycine].
 CC Overproduction of EPSP leads to glyphosate tolerance.
 CC -1- SIMILARITY: Belongs to the EPSP synthase family.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X51475; CAA35839.1; -.
 DR PIR; S12744; S12744.
 DR HSSP; P07638; 1G6S.
 DR InterPro; IPR006264; AROA.
 DR InterPro; IPR001986; EPSP_synth.
 DR Pfam; PF00275; EPSP_synthase; 1.
 DR ProDom; PD001867; EPSP_synth; 1.
 DR TIGRfam; TIGR01356; aroA; 1.
 DR PROSITE; PS00104; EPSP_SYNTHASE_1; 1.
 DR PROSITE; PS00885; EPSP_SYNTHASE_2; 1.
 DR Aromatic amino acid biosynthesis; Chloroplaest; Transferrase;
 KM Transf. peptide.
 FT TRANSIT 1 72 Chloroplaest (potential).
 FT CHAIN 73 516 carboxyvinyltransferrase.
 FT SEQUENCE 516 AA; 55030 MW; 86804B4BD8DD0F57 CRC64;
 Query Match 84.7%; Score 1911; DB 1; Length 516;
 Best Local Similarity 82.8%; Pred. No. 5.8e-123;
 Matches 367; Conservative 35; Mismatches 41; Indels 0; Gaps 0;
 QY 3 AEEVVLQPIKEISGVVKKLPGSKSLNSRIILLALSALAEFTTVNINLSSEVHYMLGALKTL 62
 DB 74 AEEVVLQPIKEISGVVKKLPGSKSLNSRIILLALSALAEFTTVNINLSSEVHYMLGALKTL 133
 QY 63 GLSVEADKAAKAAVAVVGGCGKFPVKKAKKEVQLFLGNAAGTMRSLTAATPAAGNATV 122
 DB 134 GLSVEADKAAKAAVAVVGGCGKFPVKKAKKEVQLFLGNAAGTMRSLTAATPAAGNATV 193
 QY 123 LDGVPKMERPIGDLVVGKLGADVDGFLGDCPPVAVKIGLPGGKVLGSGISSQY 182
 DB 194 LDGVPKMERPIGDLVVGKLGADVDGFLGDCPPVAVKIGLPGGKVLGSGISSQY 253
 QY 183 LSALLMAAPALAGDVEIEIIDLKISIPYEMTLRLMERFGVAEHSDSMDRPFYKGGQY 242
 DB 254 LSALLMAAPALAGDVEIEIIDLKISIPYEMTLRLMERFGVAEHSDSMDRPFYKGGQY 313
 QY 243 KSPKAAVVEGDSASVFLAGAAITGGTVVVEGCGTTLQGDVKAETLEMMGAVTTTENS 302
 DB 314 KSPKAAVVEGDSASVFLAGAAITGGTVVVEGCGTTLQGDVKAETLEMMGAVTTTENS 373
 QY 303 TSVTVTGQRPFPGRKHLKAIDVNNKMPDVAMTLAVVALFADGPTAIRDVASMKVETERN 362
 DB 374 TSVTVTGQRPFPGRKHLKAIDVNNKMPDVAMTLAVVALFADGPTAIRDVASMKVETERN 433
 QY 363 RVVAIKTELTKLGASVEEGDLVCIITPPEKLVNTAIDTYDDHRMAAFSLAACADVPVTI 422
 DB 434 RVVAIKTELTKLGASVEEGDLVCIITPPEKLVNTAIDTYDDHRMAAFSLAACADVPVTI 493
 QY 423 RDPGCTRTKTFPPYFDVLSTFVN 445

Db 494 KDBGCTRKTPDPYFOVLESITKH 516

RESULT 12

Q9FM15 PRELIMINARY; PRT; 518 AA.

AC 08M15; 01-MAR-2002 (TrEMBLrel. 20, Created)

DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE 5-enolpyruvylshikimate-3-phosphate synthase.

OS Oryzophagus violaceus.

OC Burkholderia viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosid II; Brassicales; Brassicaceae; Oryzophagus.

NCBI_TaxID=71234;

OX [1]

RP SEQUENCE FROM N.A.

RA Lin X.-F., Liu X.-J., Gou X.-S., Gao H., Deng Y.-T.,

RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

RN [2]

RA Liu X.-J., Deng Y.-T., Gao H., Gou X.-S., Wu J., Li X.-F.,

RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

CC -1- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate = phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.

CC -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway; sixth step.

CC -1- SIMILARITY: Belongs to the EPSP synthase family.

DR EMBL; AF440389; AAL65913.1; -.

DR HSP; P07638; I66S.

DR GO; GO:0003666; P:3-phosphoshikimate 1-carboxyvinyltransferase. . .; IEA.

DR GO; GO:0016740; P:transferase activity; IEA.

DR GO; GO:0016089; P:aromatic amino acid family biosynthesis, sh. . .; IEA.

DR Pfam; PF00275; EPSP synthase; 1.

DR Prodom; PD001867; EPSP_synth; 1.

DR TrEMBL; TIGR01356; arca; 1.

DR PROSITE; PS00104; EPSP SYNTHASE_1; 1.

DR PROSITE; PS00885; EPSP SYNTHASE_2; 1.

KM Amino-acid biosynthesis; Aromatic amino acid biosynthesis;

KW Transferase

SO SEQUENCE 518 AA; 55292 MW; 75C16733F594B0E0 CRC64;

Query Match 84.6%; Score 1909; DB 2; Length 518;

.Best Local Similarity 82.8%; Pred. No. 8e-123;

Matches 367; Conservative 35; Mismatches 41; Indels 0; Gaps 0;

QY 3 AEEVLTQPIKEISGVVLTGKSLNSRLILSLALSGTTVVDNLNSEDVHYMLGALKTL 62

DB 76 AEEIVLTQPIKEISGLIKLPGSKSLNSRLILSLALSGTTVVDNLNSEDVHYMLGALKTL 135

QY 63 GLSEVADKAKRAVAVVVGCGKPFVEVDAREVOLPIGNATARSITAAVTAAGNATY 122

DB 136 GLNVERDSNNRNVBEGCGIFPASVDSKSDIEVLGNATARPPLAATAAGNASTY 195

QY 123 LDGVPNRKRPIDGLVGLKQLGADVDFLTGDCPPRVKIGLPGKVKLSGSISQY 182

DB 196 LDGVPNRKRPIDGLVGLKQLGADVDFLTGDCPPRVKIGLPGKVKLSGSISQY 255

QY 183 LSLALMAAPLALDVEIEITDKLISIPYEMTILMERFVKAHSDSDRPITKGGQY 242

DB 256 LTLALMAAPLALDVEIEITDKLISIPYEMTILMERFVKAHSDSDRPITKGGQY 315

QY 243 KSPKNAVVEGDASSASYFLAAGAITGGTVVVGCGTSLGQDVKPAVEVEMGAKYTW 302

DB 316 KSPKNAVVEGDASSASYFLAAGAITGGTVVVGCGTSLGQDVKPAVEVEMGAKYTW 375

QY 303 TSVTVGPQREPRGKRLKAIIVNMNMPVANTLAVALLFADGPTAIRDVASRWYETE 362

DB 376 NSVTVGPQREPRGKRLKAIIVNMNMPVANTLAVALLFADGPTAIRDVASRWYETE 435

QY 363 RMAVIRTELTKLQASVEEGIDYCIITPPEKLVNTAIDTYDDHRMAAFSLAACADVPVTI 422

Db 436 RMAVIRTELTKLQASVEEGIDYCIITPPEKLVNTAIDTYDDHRMAAFSLAACADVPVTI 495

QY 423 RDBGCTRKTPDPYFOVLESITKH 445

Db 496 KDBGCTRKTPDPYFOVLESITKH 518

RESULT 13

Q9FVP6 PRELIMINARY; PRT; 521 AA.

AC 09FVP6; 01-MAR-2001 (TrEMBLrel. 16, Created)

DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE 5-enolpyruvylshikimate-3-phosphate (EPSP) synthase, putative (Putative 3-phosphate, putative).

GN Name=F27K7.11; Synonym=At1g48860, T24P22.2;

OS Arabidopsis thaliana (Mouse-ear cress).

OC Burkholderia viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosid II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;

OX [1]

RP SEQUENCE FROM N.A.

RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu D.,

RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Egeu P., Lee J.M.,

RA Tortum M., Yu G., Brooks S., Chao O., Chen H., Karlin-Neumann G.,

RA Kim C., Lam B., Miranda M., Nguyen M., Palm C.J., Shin P.,

RA Southwick A., Davis R.W., Becker U.R., Theologis A.,

RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu D.,

RA Maiti R., Roming C.M., Koo H., Fujii C.Y., Utecherback T.R.,

RA Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.,

RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.

RN [4]

RP SEQUENCE FROM N.A.

RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,

RA Goldsmith A.D., Lee J.M., Quach H.L., Tortum M., Yu G., Bowser L.,

RA Carrinci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,

RA Kamaya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,

RA Miranda M., Naruseka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,

RA Seki M., Shim P., Southwick A., Shinozaki K., Davis R.W., Becker U.R.,

RA Theologis A.,

RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.

CC -1- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate = phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.

CC -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway; sixth step.

CC -1- SIMILARITY: Belongs to the EPSP synthase family.

DR EMBL; AC084414; AAG29739.1; -.

DR EMBL; AY040065; AAK64123.1; -.

DR EMBL; AC084242; AAG50661.1; -.

DR EMBL; AF360224; AAK25934.1; -.

DR PIR; D96526; D96526.

DR HSP; P07638; I66S.

DR GO; GO:0003666; P:3-phosphoshikimate 1-carboxyvinyltransferase. . .; IEA.

DR GO; GO:0016740; P:transferase activity; IEA.

DR GO; GO:0016089; P:aromatic amino acid family biosynthesis, sh. . .; IEA.

DR InterPro; IPR006264; Arca_Ctrnsf.

DR InterPro; IPR001986; EPSP_synth.

DR Pfam; PF00275; EPSP synthase; 1.

DR Prodom; PD001867; EPSP_synth; 1.

DR TrEMBL; TIGR01356; arca; 1.

DR PROSITE; PS00104; EPSP SYNTHASE_1; 1.

DR PROSITE; PS00885; EPSP SYNTHASE_2; 1.

KM Amino-acid biosynthesis; Aromatic amino acid biosynthesis;
 KM Transferrase.
 SQ SEQUENCE 521 AA; 55831 MW; E2AB525FCE1A7 CRC64;

Query Match 84.1%; Score 1897; DB 2; Length 521;
 Best Local Similarity 82.2%; Pred. No. 5,4e-122;
 Matches 364; Conservative 36; Mismatches 43; Indels 0; Gaps 0;

QY 3 AEEVVLQPIKEISGVKLPKSGKSLNRIILLALAGTIVVNDLNSDDVHYMLGALKTL 62
 DB 79 ASIVVQLPIKEISGLIKLPKSGKSLNRIILLALAGTIVVNDLNSDDVHYMLGALKTL 138
 QY 63 GLSVEADKAKRAVAVVCGCGKPFVEKDAKEEVLFLGNAGTAMRSITLAAVTAAGNATYV 122
 DB 139 GLNVERHSENNRAVVEGCGVFPASIDSKSDIELYGNAGTAMRPLTAAVTAAGNATYV 198
 QY 123 LDGVPFRMRERPIGDLVVGKQLGADVDCFLGDCPEPVRYKXIGLPGKVKLSGSISSQY 182
 DB 199 LDGVPFRMRERPIGDLVVGKQLGADVDCFLGDCPEPVRYKXIGLPGKVKLSGSISSQY 258
 QY 183 LSAITLMAAPLALGDVEIEITDKLISIPYEMTLRLMERFGVAEHSDSMDRFYIKGGQKY 242
 DB 259 LRTLLMAAPLALGDVEIEITDKLISIPYEMTLRLMERFGVAEHSDSMDRFYIKGGQKY 318
 QY 243 KSPKNAVVEGDASSASYFLAGAAITGGTVVEGCGTTSLOGDVKFAVLEMMGAKYTWTE 302
 DB 319 KSPGNNAVVEGDASSASYFLAGAAITGGTVVEGCGTTSLOGDVKFAVLEMMGAKYTWTE 378
 QY 303 TSVTVTGPOREPFGKRLKALIDVNMNMKMPDAMTLAVALLFADGPTAIRDVASWRKYETE 362
 DB 379 NSVTYTGPSRDAFGMRHLRAIDVNMNMKMPDAMTLAVALLFADGPTAIRDVASWRKYETE 438
 QY 363 RMAITELTELKLGASVEEGDLCITPPEKLANVTAIDTDDHMMAMFSLAACADVPVIT 422
 DB 439 RMAITELTELKLGATVEEGSDYCVITPPKAKPAEIDTDDHMMAMFSLAACADVPVIT 498
 QY 423 RDGCTRKTPDPYFDVLTSTFVN 445
 DB 499 NDGCTRKTPDPYFDVLTSTFVN 521

RESULT 14

Q6JDVO PRELIMINARY; PRT; 514 AA.

AC Q6JDVO
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE 5-enolpyruvylshikimate-3-phosphate synthase.
 GN Name=EPSP;
 OS Brassica campestris (field mustard).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC euroids II; Brassicales; Brassicaceae; Brassica.
 OX NCBI_TaxId=3711;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Leaf;
 RA You D., Qian Y., Li X.;
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: phosphoenolpyruvate + 3-phosphoshikimate =
 CC phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.
 CC -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
 CC sixth step.
 CC -1- SIMILARITY: Belongs to the EPSP synthase family.
 DR EMBL; AY512663; AAC80163.1; -;
 DR GO; GO:0003866; F:3-phosphoshikimate-1-carboxyvinyltransferase. . .; IEA.
 DR GO; GO:0016740; F:aromatase activity; IEA.
 DR GO; GO:0016089; P:aromatase amino acid family biosynthesis, sh. . .; IEA.
 DR Interpro; IPR006264; AroA Ctranaef.
 DR Interpro; IPR001986; EPSP synth.
 DR Pfam; PF00275; EPSP synthase; 1.
 DR Prodom; PD001867; EPSP synth; 1.

DR TIGRPA6; TIGR01356; aroA; 1.
 DR PROSITE; PS00104; EPSP SYNTHASE_1; 1.
 DR PROSITE; PS00885; EPSP SYNTHASE_2; 1.
 KM Amino-acid biosynthesis; Aromatic amino acid biosynthesis;
 KM Transferrase.
 SQ SEQUENCE 514 AA; 55113 MW; AC7ADCB8FPA0301 CRC64;

Query Match 84.0%; Score 1896; DB 2; Length 514;
 Best Local Similarity 82.2%; Pred. No. 6,2e-122;
 Matches 364; Conservative 37; Mismatches 42; Indels 0; Gaps 0;

QY 3 AEEVVLQPIKEISGVKLPKSGKSLNRIILLALAGTIVVNDLNSDDVHYMLGALKTL 62
 DB 72 ASIVVQLPIKEISGLIKLPKSGKSLNRIILLALAGTIVVNDLNSDDVHYMLGALKTL 131
 QY 63 GLSVEADKAKRAVAVVCGCGKPFVEKDAKEEVLFLGNAGTAMRSITLAAVTAAGNATYV 122
 DB 132 GLNVERHSENNRAVVEGCGGIFPASIDSKSDIELYGNAGTAMRPLTAAVTAAGNATYV 191
 QY 123 LDGVPFRMRERPIGDLVVGKQLGADVDCFLGDCPEPVRYKXIGLPGKVKLSGSISSQY 182
 DB 192 LDGVPFRMRERPIGDLVVGKQLGADVDCFLGDCPEPVRYKXIGLPGKVKLSGSISSQY 251
 QY 183 LSAITLMAAPLALGDVEIEITDKLISIPYEMTLRLMERFGVAEHSDSMDRFYIKGGQKY 242
 DB 252 LRTLLMAAPLALGDVEIEITDKLISIPYEMTLRLMERFGVAEHSDSMDRFYIKGGQKY 311
 QY 243 KSPKNAVVEGDASSASYFLAGAAITGGTVVEGCGTTSLOGDVKFAVLEMMGAKYTWTE 302
 DB 312 KSPGNNAVVEGDASSASYFLAGAAITGGTVVEGCGTTSLOGDVKFAVLEMMGAKYTWTE 371
 QY 303 TSVTVTGPOREPFGKRLKALIDVNMNMKMPDAMTLAVALLFADGPTAIRDVASWRKYETE 362
 DB 372 NSVTYTGPSRDAFGMRHLRAIDVNMNMKMPDAMTLAVALLFADGPTAIRDVASWRKYETE 431
 QY 363 RMAITELTELKLGASVEEGDLCITPPEKLANVTAIDTDDHMMAMFSLAACADVPVIT 422
 DB 432 RMAITELTELKLGATVEEGSDYCVITPPKAKPAEIDTDDHMMAMFSLAACADVPVIT 491
 QY 423 RDGCTRKTPDPYFDVLTSTFVN 445
 DB 492 KDGCTRKTPDPYFDVLTSTFVN 514

RESULT 15

AR01 TOBAC STANDARD; PRT; 518 AA.

AC P23981;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DE 05-JUL-2004 (Rel. 44, Last annotation update)
 DE 3-phosphoshikimate-1-carboxyvinyltransferase 1, chloroplast precursor
 DE (EC 2.5.1.19) (5-enolpyruvylshikimate-3-phosphate synthase 1) (EPSP
 synthase 1).
 GN Name=EPSPS-1;
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC lamiales; Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxId=4097;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=92032779; PubMed=1932690;
 RA Wang Y., Jones J., Weiler S., Goldsbrough P. B.;
 RT "Expression and stability of amplified genes encoding 5-
 RT enolpyruvylshikimate-3-phosphate synthase in glycosylate-tolerant
 RT tobacco cells.";
 RL Plant Mol. Biol. 17:1127-1138 (1991).
 CC -1- CATALYTIC ACTIVITY: phosphoenolpyruvate + 3-phosphoshikimate =
 CC phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.
 CC -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
 CC sixth step.
 CC -1- SUBCELLULAR LOCATION: Chloroplast.


```
CC -1- MISCELLANEOUS: This enzyme is the target of the potent, broad-
CC spectrum herbicide, glyphosate [n-(phosphonomethyl)glycine].
CC Overproduction of EPSP leads to glyphosate tolerance.
CC -1- SIMILARITY: Belongs to the EPSP synthase family.
CC -----
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CC or send an email to license@1sb-sib.ch).
CC -----
DR EMBL; M61904; AAA34071.1; -
DR PIR; S18353; S18353.
DR HSSP; P07638; 1G6S.
DR InterPro; IPR006264; AroA.
DR InterPro; IPR001986; EPSP_synth.
DR Pfam; PF00275; EPSP_synthase; 1.
DR ProDom; PD001867; EPSP_synth; 1.
DR TIGRFAMs; TIGR01356; aroA; 1.
DR PROSITE; PS00104; EPSP_SYNTASE_1; 1.
DR PROSITE; PS00885; EPSP_SYNTASE_2; 1.
DR Aromatic amino acid biosynthesis; Chloroplast; Transferase;
KM Aromatic peptide.
FT TRANSIT 1 74 Chloroplast.
FT CHAIN 75 518 3-phosphoshikimate 1-
FT FT carboxyvinyltransferase 1.
SQ SEQUENCE 518 AA; 55711 MW; 4F03C514EAFB1681 CRC64;

Query Match 84.0%; Score 1896; DB 1; Length 518;
Best Local Similarity 82.8%; Pred. No. 6.2e-122;
Matches 365; Conservative 37; Mismatches 39; Indels 0; Gaps 0;

QY 5 EVVLQPIKEISGVVKKLPGSLSLNRIILLALAGTTVDNLNLSDEVHYMLGALTKTLG 64
DB 78 EIVLQPIKIDISGVVKKLPGSKSLNRILLALAGRTVDNLLSDDIHMYLGALTKTLG 137
QY 65 SVEADKAKRAVAVVGGCGKFPVEKAKEVQLFIGNAGTAMRSITAAVTAAGNATYVLD 124
DB 138 HVEDDNEQRAIIVEGGCGGQFPVGKSSSEELQFLGNAGTAMRPLTAAVTAAGHSRYVLD 197
QY 125 GVPFRMRERPIGDLVVGKQAGADVCEFLGTDCEPPVRVKIGLPGGKVKLSGSSISQYLS 184
DB 198 GVPFRMRERPIGDLVVGKQAGADVCEFLGTDCEPPVRIVSKGLPGGKVKLSGSSISQYLT 257
QY 185 ALLMAAFLAAGDVIEIILDKLISPIYEMTLRLMERGVKAEHSDSWDRFYIKGGQYKS 244
DB 258 ALLMAAFLAAGDVIEIILDKLISPIYEMTLRLMERGVSVSEHTSSWDKFLVRGGQYKS 317
QY 245 PKNAVVEGDASSASYFLAGAITGGTAVTEGCGTSLQGDVKKFAEVLMMGAKVTWTETS 304
DB 318 PKNAVVEGDASSASYFLAGAAVVGITVTEGCGTSLQGDVKKFAEVLKMGAEVITWETS 377
QY 305 VTYTGQREPEFGRRHLKAIDVNNMKMPDVAMTLAVALFADGPTAIRDVASWRVKETERM 364
DB 378 VTYVGPEPRNSSGMKHLAADVNNMKMPDVAMTLAVALFADGPTAIRDVASWRVKETERM 437
QY 365 VAIRTELTKLGASVEEGLDYCIITTPREKLVNTAIDTYDDHRMAAFSLAACADVPYTIKD 424
DB 438 IAICTELRLKLGATVVEGSDYCIITTPREKLVNTEIDTYDDHRMAAFSLAACADVPYTIKD 497
QY 425 PGCTRKTEPPDYFVLTSTFVKR 445
DB 498 PGCTRKTEPPDYFVLTSTFVKR 518
```


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OM protein - protein search, using SW model

Run on: September 15, 2005, 13:47:04 ; Search time 42 Seconds

(without alignment)
790.925 Million cell updates/sec

Title: US-10-803-156-7

Perfect score: 2256

Sequence: 1 AGAEEVVLQPIKISGVKL.....GCTRKTPPYFDVLSFVNK 445

Scoring table:

BLOSUM62

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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- 1: /cgn2_6/prodata/1/aa/5A_COMB.pep.*
- 2: /cgn2_6/prodata/1/aa/5B_COMB.pep.*
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- 4: /cgn2_6/prodata/1/aa/6B_COMB.pep.*
- 5: /cgn2_6/prodata/1/aa/6C_COMB.pep.*
- 6: /cgn2_6/prodata/1/aa/6D_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2256	100.0	445	US-09-800-130A-7	Sequence 7, Appl1
2	2199.5	97.5	444	US-09-243-374-5	Sequence 5, Appl1
3	2199.5	97.5	444	US-09-000-062-3	Sequence 3, Appl1
4	2199.5	97.5	444	US-08-945-144A-3	Sequence 3, Appl1
5	2198.5	97.5	444	US-09-000-062-5	Sequence 5, Appl1
6	2198.5	97.5	444	US-08-945-144A-5	Sequence 5, Appl1
7	2196.5	97.4	570	US-08-832-078-5	Sequence 5, Appl1
8	2196.5	97.4	570	US-09-698-789B-5	Sequence 5, Appl1
9	2194.5	97.3	444	US-08-476-008-56	Sequence 5, Appl1
10	2194.5	97.3	444	US-08-306-063-56	Sequence 5, Appl1
11	2194.5	97.3	444	US-08-833-485-56	Sequence 5, Appl1
12	2194.5	97.3	444	US-09-137-440-56	Sequence 5, Appl1
13	2182.5	96.7	444	US-09-137-440-56	Sequence 5, Appl1
14	2182.5	96.7	444	US-08-476-008-55	Sequence 5, Appl1
15	1927	85.4	444	US-08-306-063-55	Sequence 5, Appl1
16	1927	85.4	444	US-08-833-485-55	Sequence 5, Appl1
17	1927	85.4	444	US-09-243-374-1	Sequence 1, Appl1
18	1927	85.4	444	US-09-137-440-55	Sequence 5, Appl1
19	1915	84.9	444	US-09-137-440-55	Sequence 5, Appl1
20	1915	84.9	444	US-09-137-440-55	Sequence 5, Appl1
21	1915	84.9	444	US-09-137-440-55	Sequence 5, Appl1
22	1911	84.7	444	US-08-476-008-51	Sequence 5, Appl1
23	1911	84.7	444	US-08-306-063-51	Sequence 5, Appl1
24	1911	84.7	444	US-08-833-485-51	Sequence 5, Appl1
25	1911	84.7	444	US-09-137-440-51	Sequence 5, Appl1
26	1901	84.3	444	US-09-243-374-3	Sequence 3, Appl1
27	1898	84.1	516	US-09-800-130A-7	Patent No. 518642

28	1898	84.1	516	6	518642-4	Patent No. 518642
29	1896	84.0	444	1	US-08-476-008-53	Sequence 53, Appl1
30	1896	84.0	444	1	US-08-306-063-53	Sequence 53, Appl1
31	1896	84.0	444	1	US-08-833-485-53	Sequence 53, Appl1
32	1896	84.0	444	3	US-09-137-440-53	Sequence 53, Appl1
33	1888	83.7	444	1	US-08-476-008-52	Sequence 52, Appl1
34	1888	83.7	444	1	US-08-306-063-52	Sequence 52, Appl1
35	1888	83.7	444	1	US-08-833-485-52	Sequence 52, Appl1
36	1888	83.7	444	3	US-09-137-440-52	Sequence 52, Appl1
37	1881.5	83.4	446	3	US-09-243-374-4	Sequence 4, Appl1
38	1880	83.3	444	3	US-08-476-008-54	Sequence 54, Appl1
39	1877	83.2	444	1	US-08-306-063-54	Sequence 54, Appl1
40	1877	83.2	444	1	US-08-833-485-54	Sequence 54, Appl1
41	1877	83.2	444	3	US-09-137-440-54	Sequence 54, Appl1
42	1877	83.2	444	3	US-09-137-440-54	Sequence 54, Appl1
43	1874	83.1	444	6	5310667-3	Patent No. 5310667
44	1874	83.1	444	6	5310667-3	Patent No. 5310667
45	1869.5	82.9	446	6	5310667-4	Patent No. 5310667

ALIGNMENTS

RESULT 1									
US-09-800-130A-7									
Sequence 7, Application US/09800130A									
Patent No. 6803501									
GENERAL INFORMATION:									
APPLICANT: Baerson, Scott									
APPLICANT: Heck, Gregory									
APPLICANT: Rodriguez, Damian									
TITLE OF INVENTION: Methods for Making Plants Tolerant to Glyphosate and Compositions									
FILE REFERENCE: 60/188,093									
CURRENT FILING DATE: 2001-03-06									
NUMBER OF SEQ ID NOS: 16									
SOFTWARE: PatentIn version 3.0									
SEQ ID NO 7									
LENGTH: 445									
TYPE: PRT									
ORGANISM: Eleusine indica									
US-09-800-130A-7									
Query Match									
Best Local Similarity 100.0%; Pred. No. 2.9e-221;									
Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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DB	1	AGAEEVVLQPIKISGVKLPGSKLSNRILLSLAEGTVDNLLNSEDVHYMGALK	60						
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DB	61	TGLSVADKAKRAVAVGCGKFPVEXDAKEVOLFLGNAGTANRSLTAATAAGNAT	120						
QY	121	YVLDGVPKRRKRPVIGLVGKQLGADVDCFTGDCPPRVKVGIGLPGSKYKLSGIS	180						
DB	121	YVLDGVPKRRKRPVIGLVGKQLGADVDCFTGDCPPRVKVGIGLPGSKYKLSGIS	180						
QY	181	QYLSALMAAPALAGVVEIITDKLISIPYVMTLRIMERPVKAEHSSMDRPFYIKGQ	240						
DB	181	QYLSALMAAPALAGVVEIITDKLISIPYVMTLRIMERPVKAEHSSMDRPFYIKGQ	240						
QY	241	KYKSPKNAVVEGDASASYFLAGAAITGGTIVVEGGCTSLGQDYKFAVLEMMGAKVTM	300						
DB	241	KYKSPKNAVVEGDASASYFLAGAAITGGTIVVEGGCTSLGQDYKFAVLEMMGAKVTM	300						
QY	301	TETSVTVTPQEPKRRKRLKAIIDVNMKMPVANTLAVVAPAGGPTAIRVVASRRVVE	360						
DB	301	TETSVTVTPQEPKRRKRLKAIIDVNMKMPVANTLAVVAPAGGPTAIRVVASRRVVE	360						
QY	361	TERMAVIRTELKLGASVEGDYCIITPEKLTATAIITTDHNRMAFSIAACADVAV	420						
DB	361	TERMAVIRTELKLGASVEGDYCIITPEKLTATAIITTDHNRMAFSIAACADVAV	420						

Db 361 TERMVAIKTELKLGASVEEGDLYCIITPEKLNVTALIDTYDDHMAAFSLAACADVY 420
QY 421 TIRDPGCTRKTPPDYFDVLTSTFVN 445
Db 421 TIRDPGCTRKTPPDYFDVLTSTFVN 445

RESULT 2

US-09-243-374-5
; Sequence 5; Application US/09243374B
; Patent No. 6225114
; GENERAL INFORMATION:
; APPLICANT: Eichholtz, David Alan
; APPLICANT: Gasser, Charles Scott
; APPLICANT: Klabore, Ganesh M
; TITLE OF INVENTION: Glycoester-tolerant 5-enolpyruvyl-3-phosphoshikimate
; TITLE OF INVENTION: synthases
; FILE REFERENCE: EESP synthases
; CURRENT APPLICATION NUMBER: US/09/243,374B
; EARLIER FILING DATE: 1999-02-01
; EARLIER APPLICATION NUMBER: 07/590,647
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Zea mays
US-09-243-374-5

Query Match 97.5%; Score 2199.5; DB 3; Length 444;
Best Local Similarity 97.5%; Pred. No. 1,7e-215;
Matches 434; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

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Db 180 QYLSALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGQ 239
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Db 300 TESTSVTVGPORPEPRGRKHLKALIDVNMNKMPPVAMTLAVVALPADGPTAIRDVASRVKE 359
QY 361 TERMVAIKTELKLGASVEEGDLYCIITPEKLNVTALIDTYDDHMAAFSLAACADVY 420
Db 360 TERMVAIKTELKLGASVEEGDLYCIITPEKLNVTALIDTYDDHMAAFSLAACADVY 419
QY 421 TIRDPGCTRKTPPDYFDVLTSTFVN 445
Db 420 TIRDPGCTRKTPPDYFDVLTSTFVN 444

RESULT 3

US-09-000-062-3
; Sequence 3; Application US/09000062
; Patent No. 6338961
; GENERAL INFORMATION:
; APPLICANT: DEROSE, Richard

; APPLICANT: CHAUBERT, Nicole
; APPLICANT: GIGOT, Claude (deceased)
; TITLE OF INVENTION: ISOLATED DNA SEQUENCE CAPABLE OF SERVING AS REGULATORY
; TITLE OF INVENTION: ELEMENT IN A CHIMERIC GENE WHICH CAN BE USED FOR THE
; TITLE OF INVENTION: TRANSFORMATION OF PLANTS
; FILE REFERENCE: 022650-453
; CURRENT APPLICATION NUMBER: US/09/000,062
; EARLIER FILING DATE: 1998-05-29
; EARLIER APPLICATION NUMBER: PCT/FR96/01109
; EARLIER FILING DATE: 1996-07-17
; EARLIER APPLICATION NUMBER: FR 95/08980
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Zea mays
US-09-000-062-3

Query Match 97.5%; Score 2199.5; DB 3; Length 444;
Best Local Similarity 97.5%; Pred. No. 1,7e-215;
Matches 434; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

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Db 1 AGAEEVVLQPIKEISGVNKLPGSKLSNRILLLSALAEGETTVVDNLINSEVDHYMLGALK 60
QY 61 TLGLSVEADKAKRAVAVVCGCGKFPVE-DAKEEVOLFLGNAGTAMRSLTAAVTAAGNAT 120
Db 61 TLGLSVEADKAKRAVAVVCGCGKFPVE-DAKEEVOLFLGNAGTAMRSLTAAVTAAGNAT 119
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Db 120 YVLGVPRMRERPIGDLVGLKQLGADVDCFLGTDCPPRVVKGIGLPGKVKLSGSIS 179
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Db 120 YVLGVPRMRERPIGDLVGLKQLGADVDCFLGTDCPPRVVKGIGLPGKVKLSGSIS 179
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Db 180 QYLSALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGQ 239
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Db 360 TERMVAIKTELKLGASVEEGDLYCIITPEKLNVTALIDTYDDHMAAFSLAACADVY 419
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RESULT 4

US-08-945-144A-3
; Sequence 3; Application US/08945144A
; Patent No. 6566587
; GENERAL INFORMATION:
; APPLICANT: Lebrun, Michel
; APPLICANT: Salland, Alain
; APPLICANT: Freysinet, Georges
; APPLICANT: Degryse, Eric
; TITLE OF INVENTION: Mutated 5-Enol Pyruvylshikimate-3-Phosphate Synthase,
; TITLE OF INVENTION: Gene Coding for Said Protein and Transformed Plants
; TITLE OF INVENTION: Containing Said Gene
; FILE REFERENCE: 5500-13
; CURRENT APPLICATION NUMBER: US/08/945,144A
; EARLIER FILING DATE: 1998-01-20
; PRIOR APPLICATION NUMBER: PCT/FR96/01125

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      / PRIOR FILING DATE: 1996-07-18
      / PRIOR APPLICATION NUMBER: FRANCE 95/08979
      / PRIOR FILING DATE: 1995-07-19
      / NUMBER OF SEQ ID NOS: 15
      / SOFTWARE: PatentIn Ver. 2.0
      / SEQ ID NO 3
      / LENGTH: 444
      / TYPE: PRT
      / ORGANISM: Zea mays
      / US-08-945-144A-3

Query Match      97.5% Score 2199.5; DB 4; Length 444;
Beet Local Similarity 97.5%; Pred. No. 1.7e-215;
Matches 434; Conservative 5; Mismatch 5; Indels 1; Gaps 1;

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Db      1 AGAEIVLQPIKEISGVYKLPQSKSLNSRILLLSALAEQTVVDNLLNSEDVHYMLGALKR 60

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Db      61 TLGLSVEADKAKRAVYVVGCGGKPFVE-DAKEEVOLPLGNAQTARPLTAATAAGNAT 119

Oy      121 YLDGVPARMREPIQDLVVGKLGADVDPCFLGTDPCPVRAVKGIGLPGKRVKLSGSISS 180
Db      120 YLDGVPARMREPIQDLVVGKLGADVDPCFLGTDPCPVRAVNGIGLPGKRVKLSGSISS 179

Oy      181 QYLSALLMAAPLALGDVEIEIIDLKLSIPYEMTLRLMERGVKAEHSDSNDRFYIKGQ 240
Db      180 QYLSALLMAAPLALGDVEIEIIDLKLSIPYEMTLRLMERGVKAEHSDSNDRFYIKGQ 239

Oy      241 KYKSPKNAVVEGDSSASVYFLAGAAITGGTATTBEGCTTSLQGVKPAEVLDMGAKVTW 300
Db      240 KYKSPKNAVVEGDSSASVYFLAGAAITGGTATVBECCGTTSLQGVKPAEVLDMGAKVTW 299

Oy      301 TETSTVTVGPQREPRGRKHLKALIDVNNMKMDVAMTTLAVLLFPADGPAIRDVASWRYKE 360
Db      300 TETSTVTVGPPEPRGRHLKALIDVNNMKMDVAMTTLAVLLFPADGPAIRDVASWRYKE 359

Oy      361 TERMAVITETLTKLGASVEEGDYCIITPPEKLTANTAIQDJDHRRMAAPSLAACADVPV 420
Db      360 TERMAVITETLTKLGASVEEGDYCIITPPEKLTANTAIQDJDHRRMAAPSLAACAEVYV 419

Oy      421 TIRDPGCTRKTPPDYFDVLSFTFVN 445
Db      420 TIRDPGCTRKTPPDYFDVLSFTFVN 444

RESULT 5
US-09-000-062-5
/ Sequence 5, Application US/0900062
/ Patent No. 6338961
/ GENERAL INFORMATION:
/ APPLICANT: DEROSE, Richard
/ APPLICANT: CHAUBET, Nicole
/ APPLICANT: GIGOT, Claude (deceased)
/ TITLE OF INVENTION: ISOLATED DNA SEQUENCE CAPABLE OF SERVING AS REGULATORY
/ TITLE OF INVENTION: ELEMENT IN A CHEMIC GENE WHICH CAN BE USED FOR THE
/ TITLE OF INVENTION: TRANSFORMATION OF PLANTS
/ FILE REFERENCE: 022650-453
/ CURRENT APPLICATION NUMBER: US/09/000.062
/ CURRENT FILING DATE: 1998-05-29
/ EARLIER APPLICATION NUMBER: PCT/FR96/01109
/ EARLIER FILING DATE: 1996-07-17
/ EARLIER APPLICATION NUMBER: FR 95/08980
/ EARLIER FILING DATE: 1995-07-19
/ NUMBER OF SEQ ID NOS: 22
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 5
/ LENGTH: 444
/ TYPE: PRT
/ ORGANISM: Zea mays
/ US-09-000-062-5

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Query Match	Similarity	97.5%	Score	2198.5	DB 3	Length	444
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QY	61	TLGSLVEADKAKAAVAVGCGGKFPVEADAKEEYOLFNGNCTMRSLTAATVTAAGNAT	120				
DB	61	TLGSLVEADKAKAAVAVGCGGKFPVEADAKEEYOLFNGNCTMRSLTAATVTAAGNAT	119				
QY	121	YVLGVPFMRERPIGDLVAVGKQAGADVDFLGTDCEPVRVKYIGLPGKVKLSGIS	180				
DB	120	YVLGVPFMRERPIGDLVAVGKQAGADVDFLGTDCEPVRVNGIGLPGKVKLSGIS	179				
QY	181	QYLSALLMAAPLADGVEIEIIDKLISIPYEMTLRLMERFGVAKESDSMDREYIKGGQ	240				
DB	180	QYLSALLMAAPLADGVEIEIIDKLISIPYEMTLRLMERFGVAKESDSMDREYIKGGQ	239				
QY	241	KYKSPKAAVYEGDSSASYPFLAAGAITGGVTVEGCGTSLQGVKFAEVLEMMGAKVTW	300				
DB	240	KYKSPKAAVYEGDSSASYPFLAAGAITGGVTVEGCGTSLQGVKFAEVLEMMGAKVTW	299				
QY	301	TETSVYVTPGRBEPFRKHLKALIDVNNKMPDVAMTLAVALFADGPTAIRDVASWRKE	360				
DB	300	TETSVYVTPGRBEPFRKHLKALIDVNNKMPDVAMTLAVALFADGPTAIRDVASWRKE	359				
QY	361	TERVVAARTETLTXIGASVSEGLDVCITTPPKNLVTAIDPYDDHRMMAFSLAACAVPV	420				
DB	360	TERVVAARTETLTXIGASVSEGLDVCITTPPKNLVTAIDPYDDHRMMAFSLAACAVPV	419				
QY	421	TIRDPGCTRKTFPDYFDVLSFVFN	445				
DB	420	TIRDPGCTRKTFPDYFDVLSFVFN	444				
RESULT 6							
US-08-945-144A-5							
Sequence 5, Application US/08945144A							
Patent No. 656587							
GENERAL INFORMATION:							
APPLICANT: Lebturn, Michel							
APPLICANT: Sailand, Alain							
APPLICANT: Freysasnet, Georges							
APPLICANT: Degryse, Eric							
TITLE OF INVENTION: Mutated 5-Bno1 Pyruvylthikimate-3-Phosphate Synthase,							
TITLE OF INVENTION: Gene Coding for Said Protein and Transformed Plants							
TITLE OF INVENTION: Containing Said Gene							
FILE REFERENCES: 5500-13							
CURRENT APPLICATION NUMBER: US/08/945.144A							
CURRENT FILING DATE: 1998-01-20							
PRIOR APPLICATION NUMBER: PCT/FR96/01125							
PRIOR FILING DATE: 1996-07-18							
PRIOR APPLICATION NUMBER: FRANCE 95/08979							
PRIOR FILING DATE: 1995-07-13							
NUMBER OF SEQ ID NOS: 15							
SOFTWARE: Patentin Ver. 2.0							
SEQ ID NO 5							
LENGTH: 444							
TYPE: PRT							
ORGANISM: Zea mays							
US-08-945-144A-5							
Query Match	97.5%	Score	2198.5	DB 4	Length	444	
Best Local Similarity	97.5%	Pred. No. 2.1e-215					
Matches	434	Conservative	5	Mismatches	5	Indels	1
							Gaps 1
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DB	1	AGAEVVLQPIKEISGVVKLPGSKSLSNRIILLSALAEGLTVVDNLNSEDVHYMLGALK	60				

Qy 61 TLGLSVEADKAKRAVAVVGGCGKFPVEKDAKEEVOLFLGNAGTAMRSLTAATTAAGGNAT 120
| | | | |
Db 61 TLGLSVEADKAKRAVAVVGGCGKFPVE -DAKEEVOLFLGNAGTAMRSLTAATTAAGGNAT 119
| | | | |
Qy 121 YVLDGVPKMERBPIGDLVVGKLGADVDFLGTDGCPVAVNGIGLPGSKVLSGSIS 180
| | | | |
Db 120 YVLDGVPKMERBPIGDLVVGKLGADVDFLGTDGCPVAVNGIGLPGSKVLSGSIS 179
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Qy 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSWSMDRFYIKGQ 240
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Qy 241 KYKSPKNAVVEGDASSASYFLAGAAITGGTVVEGCGTTSLOGDVKFAEVLMMGAKVTM 300
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Db 360 TERMVAIKTELTKLGASVEEGDPYCIITPPEKLTANTAITDYDHRMAMAFSLAACADVPY 419
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Qy 421 TIRDPGCTKRTFPDYPDLSTFVKXN 445
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Db 420 TIRDPGCTKRTFPDYPDLSTFVKXN 444
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RESULT 7
US-08-832-078-5
/ Sequence 5, Application US/08832078
/ Patent No. 6040497
/ GENERAL INFORMATION:
/ APPLICANT: SPENCER, MICHAEL
/ APPLICANT: MOMM, RITA
/ APPLICANT: GWYN, JEFF
/ TITLE OF INVENTION: GLYPHOSATE RESISTANCE MAIZE LINES
/ FILE REFERENCE: DEKM:132
/ CURRENT APPLICATION NUMBER: US/08/832,078
/ NUMBER OF SEQ ID NOS: 5
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 5
/ LENGTH: 570
/ TYPE: PRF
/ ORGANISM: Artificial Sequence
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
/ OTHER INFORMATION: Primer
US-08-832-078-5

Query Match 97.4%; Score 2196.5; DB 3; Length 570;
Best Local Similarity 97.3%; Pred. No. 5.1e-215;
Matches 433; Conservative 6; Mismatches 5; Indels 1; Gaps 1;
Qy 1 AGAEEVVLQPIKEISGVVVKLPSSKSLSNRILLLSALABGTTVVDNLNSEDVHYMLGALK 60
| | | | |
Db 127 AGAEEIVLQPIKEISGVVVKLPSSKSLSNRILLLSALABGTTVVDNLNSEDVHYMLGALK 186
| | | | |
Qy 61 TLGLSVEADKAKRAVAVVGGCGKFPVEKDAKEEVOLFLGNAGTAMRSLTAATTAAGGNAT 120
| | | | |
Db 187 TLGLSVEADKAKRAVAVVGGCGKFPVE -DAKEEVOLFLGNAGTAMRSLTAATTAAGGNAT 245
| | | | |
Qy 121 YVLDGVPKMERBPIGDLVVGKLGADVDFLGTDGCPVAVNGIGLPGSKVLSGSIS 180
| | | | |
Db 246 YVLDGVPKMERBPIGDLVVGKLGADVDFLGTDGCPVAVNGIGLPGSKVLSGSIS 305
| | | | |
Qy 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSWSMDRFYIKGQ 240
| | | | |
Db 306 QYLSALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSWSMDRFYIKGQ 365
| | | | |
Qy 241 KYKSPKNAVVEGDASSASYFLAGAAITGGTVVEGCGTTSLOGDVKFAEVLMMGAKVTM 300
| | | | |

Db 366 KYKSPKNAVVEGDASSASYFLAGAAITGGTVVEGCGTTSLOGDVKFAEVLMMGAKVTM 425
| | | | |
Qy 301 TETSVTVTGPPREPGRKHLKALIDVNMNKMPPVANTLAVVALFADGPTAIRDVASRWYK 360
| | | | |
Db 426 TETSVTVTGPPREPGRKHLKALIDVNMNKMPPVANTLAVVALFADGPTAIRDVASRWYK 485
| | | | |
Qy 361 TERMVAIKTELTKLGASVEEGLDYCIITPPEKLTANTAITDYDHRMAMAFSLAACADVPY 420
| | | | |
Db 486 TERMVAIKTELTKLGASVEEGDPYCIITPPEKLTANTAITDYDHRMAMAFSLAACADVPY 545
| | | | |
Qy 421 TIRDPGCTKRTFPDYPDLSTFVKXN 445
| | | | |
Db 546 TIRDPGCTKRTFPDYPDLSTFVKXN 570
| | | | |

RESULT 8
US-09-698-789B-5
/ Sequence 5, Application US/09698789B
/ Patent No. 6762344
/ GENERAL INFORMATION:
/ APPLICANT: SPENCER, MICHAEL
/ APPLICANT: MOMM, RITA
/ APPLICANT: GWYN, J. JEFFERSON
/ APPLICANT: MCELROY, DAVID
/ APPLICANT: STEPHENS, MICHAEL A.
/ TITLE OF INVENTION: METHOD FOR PLANT BREEDING
/ FILE REFERENCE: DEKM:157USC1
/ CURRENT APPLICATION NUMBER: US/09/698,789B
/ PRIOR FILING DATE: 2000-10-07
/ PRIOR APPLICATION NUMBER: 08/927,368
/ PRIOR FILING DATE: 1997-09-11
/ PRIOR APPLICATION NUMBER: 08/899,247
/ PRIOR FILING DATE: 1997-07-23
/ NUMBER OF SEQ ID NOS: 5
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 5
/ LENGTH: 570
/ TYPE: PRF
/ ORGANISM: Zea mays
US-09-698-789B-5

Query Match 97.4%; Score 2196.5; DB 4; Length 570;
Best Local Similarity 97.3%; Pred. No. 5.1e-215;
Matches 433; Conservative 6; Mismatches 5; Indels 1; Gaps 1;
Qy 1 AGAEEVVLQPIKEISGVVVKLPSSKSLSNRILLLSALABGTTVVDNLNSEDVHYMLGALK 60
| | | | |
Db 127 AGAEEIVLQPIKEISGVVVKLPSSKSLSNRILLLSALABGTTVVDNLNSEDVHYMLGALK 186
| | | | |
Qy 61 TLGLSVEADKAKRAVAVVGGCGKFPVEKDAKEEVOLFLGNAGTAMRSLTAATTAAGGNAT 120
| | | | |
Db 187 TLGLSVEADKAKRAVAVVGGCGKFPVE -DAKEEVOLFLGNAGTAMRSLTAATTAAGGNAT 245
| | | | |
Qy 121 YVLDGVPKMERBPIGDLVVGKLGADVDFLGTDGCPVAVNGIGLPGSKVLSGSIS 180
| | | | |
Db 246 YVLDGVPKMERBPIGDLVVGKLGADVDFLGTDGCPVAVNGIGLPGSKVLSGSIS 305
| | | | |
Qy 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSWSMDRFYIKGQ 240
| | | | |
Db 306 QYLSALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSWSMDRFYIKGQ 365
| | | | |
Qy 241 KYKSPKNAVVEGDASSASYFLAGAAITGGTVVEGCGTTSLOGDVKFAEVLMMGAKVTM 300
| | | | |
Db 366 KYKSPKNAVVEGDASSASYFLAGAAITGGTVVEGCGTTSLOGDVKFAEVLMMGAKVTM 425
| | | | |
Qy 301 TETSVTVTGPPREPGRKHLKALIDVNMNKMPPVANTLAVVALFADGPTAIRDVASRWYK 360
| | | | |
Db 426 TETSVTVTGPPREPGRKHLKALIDVNMNKMPPVANTLAVVALFADGPTAIRDVASRWYK 485
| | | | |
Qy 361 TERMVAIKTELTKLGASVEEGLDYCIITPPEKLTANTAITDYDHRMAMAFSLAACADVPY 420
| | | | |
Db 486 TERMVAIKTELTKLGASVEEGDPYCIITPPEKLTANTAITDYDHRMAMAFSLAACADVPY 545
| | | | |

QY 421 TIRDPGCTRKTPDPYDVLTSTFVKN 445
DB 546 TIRDPGCTRKTPDPYDVLTSTFVKN 570

RESULT 9

US-08-476-008-56
Sequence 56, Application US/08476008
Patent No. 5627061
GENERAL INFORMATION:
APPLICANT: Barry, Gerard F.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Padgett, Stephen R.
APPLICANT: Stallings, William C.
TITLE OF INVENTION: Glycosylase Tolerant
TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
STREET: 700 Chesterfield Village Parkway
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,008
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,063
FILING DATE: 13-SEP-1994
APPLICATION NUMBER: US 07/749,611
FILING DATE: 28-AUG-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/576,537
FILING DATE: 31-AUG-1990
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(10660)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6099
TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-476-008-56

Query Match 97.3%; Score 2194.5; DB 1; Length 444;
Best Local Similarity 97.3%; Pred. No. 5.5e-215;
Matches 433; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

QY 1 AGAEEVVLQPIKISGVVVKLPGSKSLNRILLISALAEAGTTVVNDNLNSEDVHYMLGALK 60
DB 1 AGAEEVVLQPIKISGVVVKLPGSKSLNRILLISALAEAGTTVVNDNLNSEDVHYMLGALK 60
QY 61 TLGLSTVADAKAAGAAVAVVGGCGKFPVPEKDAKEYVQLFLGAGTAAAGSLTAATTAAGGAT 120
DB 61 TLGLSTVADAKAAGAAVAVVGGCGKFPVPE-DAKEEVOQLFLGAGTAAAGSLTAATTAAGGAT 119
QY 121 YVLDGVPRMRERPIGDLVGLKQLGADVDFLGTDCPPVAVKIGLPGSKVTLSSGIS 180
DB 121 YVLDGVPRMRERPIGDLVGLKQLGADVDFLGTDCPPVAVKIGLPGSKVTLSSGIS 180

DB 120 YVLDGVPRMRERPIGDLVGLKQLGADVDFLGTDCPPVAVKIGLPGSKVTLSSGIS 179
QY 181 QYISALLMAAPLALGDVEIEIIDKLISIPYEVNTLMLERFGYKAHSBMDRFFYIKGGQ 240
DB 180 QYISALLMAAPLALGDVEIEIIDKLISIPYEVNTLMLERFGYKAHSBMDRFFYIKGGQ 239
QY 241 KYKSPKNAVEGGASASVFLAGAAITGGTAVVGGCTTSLQGDVFAVLEMMGAKVM 300
DB 240 KYKSPKNAVEGGASASVFLAGAAITGGTAVVGGCTTSLQGDVFAVLEMMGAKVM 299
QY 301 TETSVTGTGPOREPFRKILKAI DVNMNKNPDAVMTLAVVALPADGPTAIRDVASRYRE 360
DB 300 TETSVTGTGPOREPFRKILKAI DVNMNKNPDAVMTLAVVALPADGPTAIRDVASRYRE 359
QY 361 TERMAVIRTELTKGASVEBGDLCITTPPEKLVNTAIDTYDDHRMAAPSLAACADV 420
DB 360 TERMAVIRTELTKGASVEBGDLCITTPPEKLVNTAIDTYDDHRMAAPSLAACADV 419
QY 421 TIRDPGCTRKTPDPYDVLTSTFVKN 445
DB 420 TIRDPGCTRKTPDPYDVLTSTFVKN 444

RESULT 10

US-08-306-063-56
Sequence 56, Application US/08306063
Patent No. 5633435
GENERAL INFORMATION:
APPLICANT: Barry, Gerard F.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Padgett, Stephen R.
APPLICANT: Stallings, William C.
TITLE OF INVENTION: Glycosylase Tolerant
TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
STREET: 700 Chesterfield Village Parkway
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/306,063
FILING DATE: 13-SEP-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,611
FILING DATE: 28-AUG-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(10660)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6047
TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-306-063-56

Query Match	97.3%	Score 2194.5;	DB 1;	Length 444;
Best Local Similarity	97.3%	Pred. No. 5.5e-215;		
Matches 433; Conservative	5;	Mismatches 6;	Indels 1;	Gaps 1;

Qy	AGAEVVLQIKISGVVTLPGSKLSNRIILLSLAGTTVVNLNSDEVHYMLGAK	60
Dp	1 AGAEVVLQIKISGVVTLPGSKLSNRIILLSLAGTTVVNLNSDEVHYMLGAKLR	60
Qy	61 TLGISVEADRAARAVVVGCGKFPVEKDAKEEVLFLGNAGTAMRSITAAVTAAGSNAT	120
Dp	61 TLGISVEADRAARAVVVGCGKFPVE-DAKEEVLFLGNAGTAMRLPITAAVTAAGSNAT	119
Qy	121 YVLDDVPRMNERIRIGYVWGLKQLGADNDCIGTCCPPVRKIGLPGGVTLSSGIS	180
Dp	120 YVLDDVPRMNERIRIGLVNGLQGLADVDCIGTCCPPVRNNGIGLPGGVTLSSGIS	179
Qy	181 QYLSALLMAAPLPLGDAVEIETIDKLISIPYEMTLRLMERGVAAEHSDSMDRPIYKGGQ	240
Dp	180 QYLSALLMAAPLPLGDAVEIETIDKLISIPYEMTLRLMERGVAAEHSDSMDRPIYKGGQ	239
Qy	241 KYKSPKNAVYEGDASSAYFLAGAAITGGTIVTEGCGTTSIQGDVKEPAEVLMMGAKATV	300
Dp	240 KYKSPKNAVYEGDASSAYFLAGAAITGGTIVTEGCGTTSIQGDVKEPAEVLMMGAKATV	299
Qy	301 TEKTSVYVTGGQRPBPRKHKLKAIDVNMNMMPVAAITLAVALLPADGPATRDVASMPVKE	360
Dp	300 TEKTSVYVTGGQRPBPRKHKLKAIDVNMNMMPVAAITLAVALLPADGPATRDVASMPVKE	359
Qy	361 TBRVVAIRTELTYLGAASVEGLDYCIITPEKLNATAIDTYDDHRMMAAFSLAACADVPV	420
Dp	360 TBRVVAIRTELTYLGAASVEGPDYCIITPEKLNATAIDTYDDHRMMAAFSLAACAEVPV	419
Qy	421 TIRDPGCTRTKTPDYVDVLTSTPKN	445
Dp	420 TIRDPGCTRTKTPDYVDVLTSTPKN	444

```

1 RESULT 11
2 US-08-833-485-56
3 ; Sequence 56, Application US/08833485
4 ; Patent No. 5804425
5
6 GENERAL INFORMATION:
7
8 APPLICANT: Barry, Gerard F.
9 APPLICANT: Kishore, Ganesh M.
10 APPLICANT: Padgett, Stephen R.
11 APPLICANT: Stallings, William C.
12 TITLE OF INVENTION: Glyphosate Tolerant
13 TITLE OF INVENTION: 5-knolpyruvylshikimate-3-Phosphate Synthases
14 NUMBER OF SEQUENCES: 69
15
16 CORRESPONDENCE ADDRESS:
17 ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. B84F
18 STREET: 700 Chesterfield Village Parkway
19 CITY: St. Louis
20 STATE: Missouri
21 COUNTRY: USA
22
23 ZIP: 63198
24
25 COMPUTER READABLE FORM:
26 MEDIUM TYPE: Floppy disk
27 COMPUTER: IBM PC compatible
28 OPERATING SYSTEM: PC-DOS/MS-DOS
29 SOFTWARE: PatentIn Release #1.0, Version #1.25
30
31 CURRENT APPLICATION DATA:
32 APPLICATION NUMBER: US/08/833,485
33 FILING DATE: 07-APR-1997
34 CLASSIFICATION: 435
35
36 PRIOR APPLICATION DATA:
37 APPLICATION NUMBER: US 08/306,063
38 FILING DATE: 13-SEP-1994
39 CLASSIFICATION: 435
40
41 PRIOR APPLICATION DATA:
42 APPLICATION NUMBER: US 07/749,611
43 FILING DATE: 28-AUG-1991
44

```

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/576,537
FILING DATE: 31-AUG-1990
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(15117)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)737-6099
TELEFAX: (314)737-6047
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-853-485-56

Query Match	97.3%	Score 2194.5;	DB 1;	Length 444;
Best Local Similarity	97.3%	Pred. No. 5.5e-215;		
Matches 433; Conservative	5;	Mismatches 6;	Indels 1;	Gaps 1;

Qy	1	AGAEVLVLOPIKEISGVNKLPGSSKSLNSRIILLLSALAEGLTVVDNLLNSBDHYMGLGAK	60
Db	1	AGAEVLVLOPIKEISGVNKLPGSSKSLNSRIILLLSALAEGLTVVDNLLNSBDHYMGLGAK	60
Qy	61	TGLGLSEADKAKARAVVVGCGKPEVEKDACEBOLEFLAGNAGTAMRSLTAAVTAAGGNAT	120
Db	61	TGLGLSEADKAKARAVVVGCGKPFVE-DAKEBVOLEFGNAGTAMRPLTAAVTAAGGNAT	119
Qy	121	YVLDDGVRRRREPIDDLVLGKLKQJGADVDCETLGDPCPPVVKIGLPGKRYLSSGIS	180
Db	120	YVLDDGVRRRREPIDDLVLGKLKQJGADVDCETLGDPCPPVRNNGIGLPGKRYLSSGIS	179
Qy	181	QYLSALIMAAAPALGDVEIEIIDLKLSIPYEMTLRLMERFGVAAEHSDSMDRFYIKGQ	240
Db	180	QYLSALIMAAAPPLGDVEIEIIDLKLSIPYEMTLRLMERFGVAAEHSDSMDRFYIKGQ	239
Qy	241	KYKSPKNAVVEGDASASYPLAGAATGGTIVTVEGCGTSLIQGDVKEFAYLEMMGAKVTM	300
Db	240	KYKSPKNAVVEGDASASYPFLAGAATGGTIVTVEGCGTSLQGDVKEFAYLEMMGAKVTM	299
Qy	301	TEKTSVTVGPOEPPBGRGHILKAIDVNNMKMDVMATLVAVALPADGETALRDVAASRYVE	360
Db	300	TEKTSVTVGPPBPPBGRGHILKAIDVNNMKMDVMATLVAVALPADGETALRDVAASRYVE	359
Qy	361	TERHVAIRIELTKLGASVEBGLDYCIITPEPKLVNTAIDTYDDHRMAAFSLAACADVPV	420
Db	360	TERHVAIRIELTKLGASVEBGPDYCIITPEPKLVNTAIDTYDDHRMAAFSLAACAEVPV	419
Qy	421	TIIRDPCETKTPEDYFDVLSTPVKN	445
Db	420	TIIRDPCETKTPEDYFDVLSTPVKN	444

RESULT 12
US-09-137-440-56
Sequence 56, Application US/09137440
Patent No. 624876
GENERAL INFORMATION:
APPLICANT: Barry, Gerard F.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Padgett, Stephen R.
APPLICANT: Scilling, William C.
TITLE OF INVENTION: Glyphosate Tolerant
TITLE OF INVENTION: 5-Ethylpyruvylshikimate-3-Phosphate Synthases
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BBAF
STREET: 700 Chesterfield Village Parkway
CITY: St. Louis

STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/137,440
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/833,485
FILING DATE: 07-APR-1997
APPLICATION NUMBER: US 08/306,063
FILING DATE: 13-SEP-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/749,611
FILING DATE: 28-AUG-1991
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/576,537
FILING DATE: 31-AUG-1990
ATTORNEY/AGENT INFORMATION:
NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21 (15117) A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)737-6099
TELEFAX: (314)737-6047
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-137-440-56

Query Match 97.3%; Score 2194.5; DB 3; Length 444;
Best Local Similarity 97.3%; Pred. No. 5.5e-215;
Matches 433; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

QY 1 AGAEEVVLQPIKISGVVLPKSKLSNNRLLLSALAEGETVVDNLNSDHYHMGALX 60
DB 1 AGAEEVVLQPIKISGVVLPKSKLSNNRLLLSALAEGETVVDNLNSDHYHMGALX 60
QY 61 TLGLSVADKAAKRAVAVVCGGKFPVEKDAKEEVQLFLNAGTAMRSLTAAVTAAGNAT 120
DB 61 TLGLSVADKAAKRAVAVVCGGKFPVE -DAKEEVQLFLNAGTAMRSLTAAVTAAGNAT 119
QY 121 YVLGVPRRRERPIGDLVVGKQLGADVDCFLGTDCPPRVKGIIGLPGKVKLSGSISS 180
DB 121 YVLGVPRRRERPIGDLVVGKQLGADVDCFLGTDCPPRVKGIIGLPGKVKLSGSISS 179
QY 181 QYLSALMAAPLALGVEIEIIDKLSIPYEMTLRLMERFGVKAHSDSMDFYIKGQ 240
DB 180 QYLSALMAAPLALGVEIEIIDKLSIPYEMTLRLMERFGVKAHSDSMDFYIKGQ 239
QY 241 KYKSPNAAVEGDASASYFLAGAAITGGTVVVEGCGTSLQGVKFAEVLMMGAKVTW 300
DB 240 KYKSPNAAVEGDASASYFLAGAAITGGTVVVEGCGTSLQGVKFAEVLMMGAKVTW 299
QY 301 TETSVTVTGPQREPPGRKHLKAI DVNMNMKPDVAMTLAVVALPADGPTAIRVASVRVKE 360
DB 300 TETSVTVTGPQREPPGRKHLKAI DVNMNMKPDVAMTLAVVALPADGPTAIRVASVRVKE 359
QY 361 TERMVAIRTELTKLGSVSEGLDYCIITPEKLNVTAIIDYDHRMAAFSLAACAEVVP 420
DB 360 TERMVAIRTELTKLGSVSEGLDYCIITPEKLNVTAIIDYDHRMAAFSLAACAEVVP 419
QY 421 TIRDPCTRKTTPDPYDVLSTFVN 445
DB 420 TIRDPCTRKTTPDPYDVLSTFVN 444

RESULT 13
5310667-5
/ Patent No. 5310667
/ APPLICANT: EICHHOLTZ, DAVID A.; GASSER, CHARLES S.; KISHORE,
/ GANESH M.
/ TITLE OF INVENTION: GLYPHOSATE-TOLERANT 5-ENOLPYRUVYL
/ -3-PHOSPHOSHIKIMATE SYNTHASES
/ NUMBER OF SEQUENCES: 37
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/07/380,963
/ FILING DATE: 17-JUL-1989
/ SEQ ID NO: 5
/ LENGTH: 444
5310667-5

Query Match 96.7%; Score 2182.5; DB 6; Length 444;
Best Local Similarity 96.9%; Pred. No. 9.1e-214;
Matches 431; Conservative 6; Mismatches 7; Indels 1; Gaps 1;

QY 1 AGAEEVVLQPIKISGVVLPKSKLSNNRLLLSALAEGETVVDNLNSDHYHMGALX 60
DB 1 AGAEEVVLQPIKISGVVLPKSKLSNNRLLLSALAEGETVVDNLNSDHYHMGALX 60
QY 61 TLGLSVADKAAKRAVAVVCGGKFPVEKDAKEEVQLFLNAGTAMRSLTAAVTAAGNAT 120
DB 61 TLGLSVADKAAKRAVAVVCGGKFPVE -DAKEEVQLFLNAGTAMRSLTAAVTAAGNAT 119
QY 121 YVLGVPRRRERPIGDLVVGKQLGADVDCFLGTDCPPRVKGIIGLPGKVKLSGSISS 180
DB 121 YVLGVPRRRERPIGDLVVGKQLGADVDCFLGTDCPPRVKGIIGLPGKVKLSGSISS 179
QY 181 QYLSALMAAPLALGVEIEIIDKLSIPYEMTLRLMERFGVKAHSDSMDFYIKGQ 240
DB 180 QYLSALMAAPLALGVEIEIIDKLSIPYEMTLRLMERFGVKAHSDSMDFYIKGQ 239
QY 241 KYKSPNAAVEGDASASYFLAGAAITGGTVVVEGCGTSLQGVKFAEVLMMGAKVTW 300
DB 240 KYKSPNAAVEGDASASYFLAGAAITGGTVVVEGCGTSLQGVKFAEVLMMGAKVTW 299
QY 301 TETSVTVTGPQREPPGRKHLKAI DVNMNMKPDVAMTLAVVALPADGPTAIRVASVRVKE 360
DB 301 TETSVTVTGPQREPPGRKHLKAI DVNMNMKPDVAMTLAVVALPADGPTAIRVASVRVKE 359
QY 361 TERMVAIRTELTKLGSVSEGLDYCIITPEKLNVTAIIDYDHRMAAFSLAACAEVVP 420
DB 360 TERMVAIRTELTKLGSVSEGLDYCIITPEKLNVTAIIDYDHRMAAFSLAACAEVVP 419
QY 421 TIRDPCTRKTTPDPYDVLSTFVN 445
DB 420 TIRDPCTRKTTPDPYDVLSTFVN 444

RESULT 14
5310667-5
/ Patent No. 5310667
/ APPLICANT: EICHHOLTZ, DAVID A.; GASSER, CHARLES S.; KISHORE,
/ GANESH M.
/ TITLE OF INVENTION: GLYPHOSATE-TOLERANT 5-ENOLPYRUVYL
/ -3-PHOSPHOSHIKIMATE SYNTHASES
/ NUMBER OF SEQUENCES: 37
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/07/380,963
/ FILING DATE: 17-JUL-1989
/ SEQ ID NO: 5
/ LENGTH: 444
5310667-5

Query Match 96.7%; Score 2182.5; DB 6; Length 444;
Best Local Similarity 96.9%; Pred. No. 9.1e-214;
Matches 431; Conservative 6; Mismatches 7; Indels 1; Gaps 1;


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QY      1 AGAEVVLQPIKEISGVVLPKSGKSLSNRIILLSALAEGLTVVDNLNSDEVHYMLGALK 60
      1 AGAEVILQPIKEISGVVLPKSGKSLSNRIILLSALAEGLTVVDNLNSDEVHYMLGALK 60
DB      61 TLGLSVADKAAKRAVAVVCGGKFPVEKDAKEEVQFLGNAGTAMRSLTAATTAAGNAT 120
QY      61 TLGLSVADKAAKRAVAVVCGGKFPVEKDAKEEVQFLGNAGTAMRSLTAATTAAGNAT 120
DB      61 TLGLSVADKAAKRAVAVVCGGKFPVEKDAKEEVQFLGNAGTAMRSLTAATTAAGNAT 119
QY      121 YVLDGVPKRRERIGDLVGLKQLGADVDCFLGTDCPPRVAVNGISGLPGKVKLSGISISS 179
DB      120 YVLDGVPKRRERIGDLVGLKQLGADVDCFLGTDCPPRVAVNGISGLPGKVKLSGISISS 179
QY      181 QYLSALMAAPLALGVEIEIIDLKLSIPYVENTLRLMERFGVKAHSDSWDRFYIKGGQ 240
DB      180 QYLSALMAAPLALGVEIEIIDLKLSIPYVENTLRLMERFGVKAHSDSWDRFYIKGGQ 239
QY      241 KYKSPKNAAYEGDASSAFYLAGAATGGTVYEGCGTSSLOGDVKFAEYLEMMGAKVTM 300
DB      240 KYKSPKNAAYEGDASSAFYLAGAATGGTVYEGCGTSSLOGDVKFAEYLEMMGAKVTM 299
QY      301 TETSUVTGTGPORBPGRKHLKALDVNMNMKMPDVAMTLAVVALPADGPTAIRDVASRVKYE 360
DB      300 TETSUVTGTGPORBPGRKHLKALDVNMNMKMPDVAMTLAVVALPADGPTAIRDVASRVKYE 359
QY      361 TERMAVIRTELTKLGASVEEGLDYCIITPPEKLNVTALDYYDDHRMAAFSLAACADVPY 420
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RESULT 15

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US-08-476-008-55
; Sequence 55, Application US/08476008
; Patent No. 5627061
; GENERAL INFORMATION:
; APPLICANT: Barry, Gerard F.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Padgett, Stephen M.
; APPLICANT: Stallings, William C.
; TITLE OF INVENTION: Glycosylase Tolerant
; TITLE OF INVENTION: 5-Ethylpyruvylshikimate-3-Phosphate Synthases
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BBAF
; STREET: 700 Chesterfield Village Parkway
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,008
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/306,063
; FILING DATE: 13-SEP-1994
; APPLICATION NUMBER: US 07/749,611
; FILING DATE: 28-AUG-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/576,537
; FILING DATE: 31-AUG-1990
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoerner Jr., Dennis R.

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; REGISTRATION NUMBER: 30, 914
; REFERENCE/DOCKET NUMBER: 38-21(10660)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)537-6099
; TELEFAX: (314)537-6047
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-476-008-55

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Query Match      85.4%; Score 1927; DB 1; Length 444;
Best Local Similarity 84.4%; Pred No. 1,1e-187;
Matches 312; Conservative 31; Mismatches 38; Indels 0; Gaps 0;

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QY      65 SVADKAAKRAVAVVCGGKFPVEKDAKEEVQFLGNAGTAMRSLTAATTAAGNATYVLD 124
DB      64 HVEBDSANQRAVAVVCGGKFPVKGESKEBIQLFLGNAGTAMRPLTAATTAAGNSRYVLD 123
QY      125 GVPRRRERPIGDLVGLKQLGADVDCFLGTDCPPRVAVNGISGLPGKVKLSGISISSOYLS 184
DB      124 GVPRRRERPIGDLVGLKQLGADVDCFLGTDCPPRVAVNGISGLPGKVKLSGISISSOYLT 183
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QY      305 VTVGTGPORBPGRKHLKALDVNMNMKMPDVAMTLAVVALPADGPTAIRDVASRVKETERM 364
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QY      365 VAIRTELTKLGASVEEGLDYCIITPPEKLNVTALDYYDDHRMAAFSLAACADVPVTVTD 424
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Search completed: September 15, 2005, 13:57:08
Job time : 44 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 15, 2005, 13:55:40 ; Search time 185 Seconds
(without alignments)
974.015 Million cell updates/sec

Title: US-10-803-156-7

Perfect score: 2256

Sequence: 1 AGAEEVVLQPIKEISGVVL.....GCTRKTPFPYFDVLSFVKN 445

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1812044 seqs, 404927589 residues

Total number of hits satisfying chosen parameters: 1812044

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA:*
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22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2256	100.0	445	10 US-09-800-130A-7	Sequence 7, Appl1
2	2256	100.0	445	14 US-10-413-909-7	Sequence 7, Appl1
3	2256	100.0	445	18 US-10-803-156-7	Sequence 7, Appl1
4	2199.5	97.5	444	14 US-10-023-833-3	Sequence 7, Appl1
5	2199.5	97.5	444	14 US-10-214-766-22	Sequence 22, Appl1
6	2199.5	97.5	444	20 US-11-051-955-28	Sequence 28, Appl1
7	2198.5	97.5	444	14 US-10-023-833-5	Sequence 3, Appl1
8	2196.5	97.4	570	17 US-10-869-324-5	Sequence 5, Appl1
9	2194.5	97.3	444	9 US-11-050-645-5	Sequence 5, Appl1
10	2194.5	97.3	444	9 US-09-861-696-56	Sequence 56, Appl1
11	2194.5	97.3	444	9 US-09-464-099A-56	Sequence 56, Appl1

12	2165	96.0	515	16 US-10-437-963-162988	Sequence 162988, Appl1
13	1929	85.5	391	14 US-10-214-766-20	Sequence 20, Appl1
14	1927	85.4	444	9 US-09-861-696-55	Sequence 55, Appl1
15	1927	85.4	444	9 US-09-464-099A-55	Sequence 55, Appl1
16	1927	85.4	516	14 US-10-214-766-24	Sequence 24, Appl1
17	1927	85.4	516	20 US-11-051-955-27	Sequence 27, Appl1
18	1918	85.0	516	10 US-09-791-489-9	Sequence 9, Appl1
19	1911	84.7	444	9 US-09-861-696-51	Sequence 51, Appl1
20	1911	84.7	444	9 US-09-464-099A-51	Sequence 51, Appl1
21	1911	84.7	516	14 US-10-214-766-28	Sequence 28, Appl1
22	1911	84.7	516	20 US-11-051-955-26	Sequence 26, Appl1
23	1898	84.1	534	15 US-10-424-599-194746	Sequence 194746, Appl1
24	1897	84.1	521	14 US-10-214-766-26	Sequence 26, Appl1
25	1896	84.0	444	9 US-09-861-696-53	Sequence 53, Appl1
26	1896	84.0	444	9 US-09-464-099A-53	Sequence 53, Appl1
27	1888	83.7	444	9 US-09-861-696-52	Sequence 52, Appl1
28	1888	83.7	520	14 US-10-214-766-27	Sequence 27, Appl1
29	1888	83.7	520	20 US-11-051-955-2	Sequence 2, Appl1
30	1888	83.7	444	9 US-09-464-099A-54	Sequence 54, Appl1
31	1877	83.2	444	9 US-10-214-766-45	Sequence 45, Appl1
32	1877	83.2	520	14 US-10-214-766-25	Sequence 25, Appl1
33	1877	83.2	347	14 US-10-214-766-21	Sequence 21, Appl1
34	1664	73.8	338	14 US-10-214-766-23	Sequence 23, Appl1
35	1490	66.0	248	15 US-10-425-114-43334	Sequence 43334, Appl1
36	1264	56.0	424	14 US-10-214-766-45	Sequence 45, Appl1
37	118.5	49.6	426	14 US-10-214-766-43	Sequence 43, Appl1
38	111.6	49.5	427	9 US-09-861-696-59	Sequence 59, Appl1
39	111.5	49.4	427	9 US-09-464-099A-59	Sequence 59, Appl1
40	111.5	49.4	427	14 US-10-214-766-46	Sequence 46, Appl1
41	111.5	49.2	427	15 US-10-369-493-783	Sequence 783, Appl1
42	1109.5	49.2	427	9 US-09-861-696-60	Sequence 60, Appl1
43	1108	49.1	427	9 US-09-464-099A-60	Sequence 60, Appl1
44	1108	49.1	427	14 US-10-214-766-44	Sequence 44, Appl1
45	1108	49.1	427	14 US-10-214-766-44	Sequence 44, Appl1

ALIGNMENTS

RESULT 1
US-09-800-130A-7
; Sequence 7, Appl1 Application US/09800130A
; Publication No. US20030188346A1
; GENERAL INFORMATION:
; APPLICANT: Baerson, Scott
; APPLICANT: Heck, Gregory
; APPLICANT: Rodriguez, Damian
; TITLE OF INVENTION: Methods for Making Plants Tolerant to Glyphosate and Compositions
; FILE REFERENCE: 60/188,093
; CURRENT APPLICATION NUMBER: US/09/800,130A
; CURRENT FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 7
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Eleusine indica
US-09-800-130A-7

Query Match	100.0%	Score 2256	DB 10	Length 445
Best Local Similarity	100.0%	Pred. No. 3.8e-199		
Matches 445	Conservative 0	Mismatches 0	Indels 0	Gaps 0
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DB	1	AGAEEVVLQPIKEISGVVLPGSKSLSNRIILSLAEGTVVDMLNSEDVHMLGALK	60	
QY	61	TIGLSVADKAKRAVVGCGGKFPYEDKAEVQLFLGAGTAKRSLLTAATTAAGGANT	120	
DB	61	TIGLSVADKAKRAVVGCGGKFPYEDKAEVQLFLGAGTAKRSLLTAATTAAGGANT	120	
QY	121	YTLGDPVRRREPIGLDVLVGLKGLADVDCFLGTGDCPPRVKVGIGLPGGKYLGSSTIS	180	

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Db      121  YVLDGVPNRMRERPIGDLVVGKLGADVDCFLGTDCEPVRVKIGLPGSKVYLSGSIS 180
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Db      301  TETSVTVTGQREPFGRKHLKAIIDVNMNMPDVAMTLAVVALPADGPTAIRDVASWRVKE 360
Qy      361  TERMVAIRTELTKLGASVEEGLDYCIITPPEKLVNTAIDTYDDHRMAMAFSLAACADVPV 420
Db      361  TERMVAIRTELTKLGASVEEGLDYCIITPPEKLVNTAIDTYDDHRMAMAFSLAACADVPV 420
Qy      421  TIRDPGCTRKTPPDYFDVLSFVK 445
Db      421  TIRDPGCTRKTPPDYFDVLSFVK 445

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RESULT 2
US-10-413-909-7
; Sequence 7, Application US/10413909
; Publication No. US20030192072A1
; GENERAL INFORMATION:
; APPLICANT: Baerson, Scott
; APPLICANT: Heck, Gregory
; APPLICANT: Rodriguez, Damian
; TITLE OF INVENTION: Methods for Making Plants Tolerant to Glyphosate and Compositions
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 11898.0019.00DVUS01 (MOBS019--1)
; CURRENT APPLICATION NUMBER: US/10/413,909
; CURRENT FILING DATE: 2003-04-15
; PRIOR APPLICATION NUMBER: 60/188,093
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 445
; TYPE: PR
; ORGANISM: Eleusine indica
US-10-413-909-7

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Query Match      100.0%; Score 2256; DB 14; Length 445;
Best Local Similarity 100.0%; Pred. No. 3,8e-199;
Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      61  TLGLSVEADKAAKRAVYVVGCGKFPVEKDACEVQVFLGNAGTMRSLTAATTAAGNAT 120
Db      61  TLGLSVEADKAAKRAVYVVGCGKFPVEKDACEVQVFLGNAGTMRSLTAATTAAGNAT 120
Qy      121  YVLDGVPNRMRERPIGDLVVGKLGADVDCFLGTDCEPVRVKIGLPGSKVYLSGSIS 180
Db      121  YVLDGVPNRMRERPIGDLVVGKLGADVDCFLGTDCEPVRVKIGLPGSKVYLSGSIS 180
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Qy      241  KYKSPKNAAYVEGDASSASYFLAGAAITGGTVVEGCGTISLOGDVKFAVLEMMGAKVTM 300
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Db      301  TETSVTVTGQREPFGRKHLKAIIDVNMNMPDVAMTLAVVALPADGPTAIRDVASWRVKE 360

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Qy      361  TERMVAIRTELTKLGASVEEGLDYCIITPPEKLVNTAIDTYDDHRMAMAFSLAACADVPV 420
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RESULT 3
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; Sequence 7, Application US/10803156
; Publication No. US20040148650A1
; GENERAL INFORMATION:
; APPLICANT: Baerson, Scott
; APPLICANT: Heck, Gregory
; APPLICANT: Rodriguez, Damian
; TITLE OF INVENTION: Methods for Making Plants Tolerant to Glyphosate and Compositions
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 11898.0019.00DVUS02 (MOBS019--2)
; CURRENT APPLICATION NUMBER: US/10/803,156
; CURRENT FILING DATE: 2004-03-17
; PRIOR APPLICATION NUMBER: 60/188,093
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: 09/800,130
; PRIOR FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 445
; TYPE: PR
; ORGANISM: Eleusine indica
US-10-803-156-7

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Query Match      100.0%; Score 2256; DB 18; Length 445;
Best Local Similarity 100.0%; Pred. No. 3,8e-199;
Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  AGAEEVVLQPIKEISGVVYKLGSKSLSNRIILLSALAGTTVVDNLNSEDVHYMLGALK 60
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Db      61  TLGLSVEADKAAKRAVYVVGCGKFPVEKDACEVQVFLGNAGTMRSLTAATTAAGNAT 120
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Db      121  YVLDGVPNRMRERPIGDLVVGKLGADVDCFLGTDCEPVRVKIGLPGSKVYLSGSIS 180
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Db      181  QYLSALIMAAPLALGDVEIEIIDKLISIPYEMTLRMRFGVKASHSDSMRPFYIKGQ 240
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Db      241  KYKSPKNAAYVEGDASSASYFLAGAAITGGTVVEGCGTISLOGDVKFAVLEMMGAKVTM 300
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Qy      361  TERMVAIRTELTKLGASVEEGLDYCIITPPEKLVNTAIDTYDDHRMAMAFSLAACADVPV 420
Db      361  TERMVAIRTELTKLGASVEEGLDYCIITPPEKLVNTAIDTYDDHRMAMAFSLAACADVPV 420
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RESULT 4

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; Sequence 3, Application US/10023839
; Publication No. US20030027312A1
; GENERAL INFORMATION:
; APPLICANT: DEROSE, Richard
; APPLICANT: CHAUBERT, Nicole
; APPLICANT: GIGOT, Claude (deceased)
; TITLE OF INVENTION: ISOLATED DNA SEQUENCE CAPABLE OF SERVING AS REGULATORY
; TITLE OF INVENTION: ELEMENT IN A CHIMERIC GENE WHICH CAN BE USED FOR THE
; TITLE OF INVENTION: TRANSFORMATION OF PLANTS
; FILE REFERENCE: 022550-453
; CURRENT APPLICATION NUMBER: US/10/023,839
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/000,062
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: FR 95/08980
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Zea mays
US-10-023-839-3

Query Match      97.5%; Score 2199.5; DB 14; Length 444;
Best Local Similarity 97.5%; Pred. No. 6.3e-194;
Matches 444; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

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DB      120 YVLGVPRMRERPIGDLVVGKQLGADVDCFLGTDCPPVRVNGIGLPGKVKLSGSISS 179
        120 YVLGVPRMRERPIGDLVVGKQLGADVDCFLGTDCPPVRVNGIGLPGKVKLSGSISS 179
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        181 QYLSALMAAPLALGDVEIEIIDKLSIPYVENTLRLMERFGVKAHSDSMRPFYIKGQ 240
DB      180 QYLSALMAAPLALGDVEIEIIDKLSIPYVENTLRLMERFGVKAHSDSMRPFYIKGQ 239
        180 QYLSALMAAPLALGDVEIEIIDKLSIPYVENTLRLMERFGVKAHSDSMRPFYIKGQ 239
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DB      240 KXSPFNNAVVEGDASASAYFLAGAAITGGTVVVEGCGTTSLOGDVKFAVLEMMGAKVTM 299
        240 KXSPFNNAVVEGDASASAYFLAGAAITGGTVVVEGCGTTSLOGDVKFAVLEMMGAKVTM 299
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        301 TETSVTVTGPOREPFRGRKHLKALDVNMNMKMPDVANTLAVVALFADGPTAIRDVASMRVKE 360
DB      300 TETSVTVTGPOREPFRGRKHLKALDVNMNMKMPDVANTLAVVALFADGPTAIRDVASMRVKE 359
        300 TETSVTVTGPOREPFRGRKHLKALDVNMNMKMPDVANTLAVVALFADGPTAIRDVASMRVKE 359
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        361 TERMAAIRTELTKLGASVEEGDLYCIITPPEKLTNTAIDTYDDHRMAAFSLAACADVIV 420
DB      360 TERMAAIRTELTKLGASVEEGDLYCIITPPEKLTNTAIDTYDDHRMAAFSLAACADVIV 419
        360 TERMAAIRTELTKLGASVEEGDLYCIITPPEKLTNTAIDTYDDHRMAAFSLAACADVIV 419
QY      421 TIRDPGCTRKTPPDYFDVLTSTFVN 445
        421 TIRDPGCTRKTPPDYFDVLTSTFVN 445
DB      420 TIRDPGCTRKTPPDYFDVLTSTFVN 444
        420 TIRDPGCTRKTPPDYFDVLTSTFVN 444

RESULT 5
US-10-214-766-22
; Sequence 22, Application US/10214766
; Publication No. US20030084473A1
; GENERAL INFORMATION:
; APPLICANT: Gocal, Greg
; TITLE OF INVENTION: NON-TRANSGENIC HERBICIDE RESISTANT PLANTS
; FILE REFERENCE: CA1138
; CURRENT APPLICATION NUMBER: US/10/214,766
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,734
```

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; PRIOR FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Zea mays
US-10-214-766-22

Query Match      97.5%; Score 2199.5; DB 14; Length 444;
Best Local Similarity 97.5%; Pred. No. 6.3e-194;
Matches 444; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

QY      1 AGAEEVVLQPIKEISGVVVLPGSKSLSNRIILLSALAEGETTVVDNLINSEDVHYMLGALK 60
        1 AGAEEVVLQPIKEISGVVVLPGSKSLSNRIILLSALAEGETTVVDNLINSEDVHYMLGALK 60
DB      61 TLGLSVADKAAKRAVAVVCGGKFPVE-DAKEEVQFLGNAGTAMRPLTAATTAAGNAT 119
        61 TLGLSVADKAAKRAVAVVCGGKFPVE-DAKEEVQFLGNAGTAMRPLTAATTAAGNAT 119
QY      121 YVLGVPRMRERPIGDLVVGKQLGADVDCFLGTDCPPVRVNGIGLPGKVKLSGSISS 180
        121 YVLGVPRMRERPIGDLVVGKQLGADVDCFLGTDCPPVRVNGIGLPGKVKLSGSISS 180
DB      120 YVLGVPRMRERPIGDLVVGKQLGADVDCFLGTDCPPVRVNGIGLPGKVKLSGSISS 179
        120 YVLGVPRMRERPIGDLVVGKQLGADVDCFLGTDCPPVRVNGIGLPGKVKLSGSISS 179
QY      181 QYLSALMAAPLALGDVEIEIIDKLSIPYVENTLRLMERFGVKAHSDSMRPFYIKGQ 240
        181 QYLSALMAAPLALGDVEIEIIDKLSIPYVENTLRLMERFGVKAHSDSMRPFYIKGQ 240
DB      180 QYLSALMAAPLALGDVEIEIIDKLSIPYVENTLRLMERFGVKAHSDSMRPFYIKGQ 239
        180 QYLSALMAAPLALGDVEIEIIDKLSIPYVENTLRLMERFGVKAHSDSMRPFYIKGQ 239
QY      241 KXSPFNNAVVEGDASASAYFLAGAAITGGTVVVEGCGTTSLOGDVKFAVLEMMGAKVTM 300
        241 KXSPFNNAVVEGDASASAYFLAGAAITGGTVVVEGCGTTSLOGDVKFAVLEMMGAKVTM 300
DB      240 KXSPFNNAVVEGDASASAYFLAGAAITGGTVVVEGCGTTSLOGDVKFAVLEMMGAKVTM 299
        240 KXSPFNNAVVEGDASASAYFLAGAAITGGTVVVEGCGTTSLOGDVKFAVLEMMGAKVTM 299
QY      301 TETSVTVTGPOREPFRGRKHLKALDVNMNMKMPDVANTLAVVALFADGPTAIRDVASMRVKE 360
        301 TETSVTVTGPOREPFRGRKHLKALDVNMNMKMPDVANTLAVVALFADGPTAIRDVASMRVKE 360
DB      300 TETSVTVTGPOREPFRGRKHLKALDVNMNMKMPDVANTLAVVALFADGPTAIRDVASMRVKE 359
        300 TETSVTVTGPOREPFRGRKHLKALDVNMNMKMPDVANTLAVVALFADGPTAIRDVASMRVKE 359
QY      361 TERMAAIRTELTKLGASVEEGDLYCIITPPEKLTNTAIDTYDDHRMAAFSLAACADVIV 420
        361 TERMAAIRTELTKLGASVEEGDLYCIITPPEKLTNTAIDTYDDHRMAAFSLAACADVIV 420
DB      360 TERMAAIRTELTKLGASVEEGDLYCIITPPEKLTNTAIDTYDDHRMAAFSLAACADVIV 419
        360 TERMAAIRTELTKLGASVEEGDLYCIITPPEKLTNTAIDTYDDHRMAAFSLAACADVIV 419
QY      421 TIRDPGCTRKTPPDYFDVLTSTFVN 445
        421 TIRDPGCTRKTPPDYFDVLTSTFVN 445
DB      420 TIRDPGCTRKTPPDYFDVLTSTFVN 444
        420 TIRDPGCTRKTPPDYFDVLTSTFVN 444

RESULT 6
US-11-051-955-28
; Sequence 28, Application US/11051955
; Publication No. US20050177899A1
; GENERAL INFORMATION:
; APPLICANT: Beetnam, P.
; APPLICANT: Alesar, P.
; APPLICANT: Walker, K.
; APPLICANT: Metz, R.
; TITLE OF INVENTION: NON-TRANSGENIC HERBICIDE RESISTANT PLANTS
; FILE REFERENCE: 7991-086
; CURRENT APPLICATION NUMBER: US/11/051,955
; CURRENT FILING DATE: 2005-02-04
; PRIOR APPLICATION NUMBER: US/09/685,403
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: 60/158,027
; PRIOR FILING DATE: 1999-10-07
; PRIOR APPLICATION NUMBER: 60/173,564
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Zea mays
US-11-051-955-28
```

Query Match 97.5%; Score 2199.5; DB 20; Length 444;
Best Local Similarity 97.5%; Pred. No. 6.3e-194;
Matches 434; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

QY 1 AGAEEVVLQPIKEISGVVYKLPKSKLSNRILLLSALAEGLTVVDNLINSEDVHYMLGALK 60
DB 1 AGAEEIVLQPIKEISGVVYKLPKSKLSNRILLLSALAEGLTVVDNLINSEDVHYMLGALK 60
QY 61 TLGLSVEADKAAKRAVAVVGGCGKFPVE-DAKEEVOLFLGNAGTAMRSILTAATAAGNAT 120
DB 61 TLGLSVEADKAAKRAVAVVGGCGKFPVE-DAKEEVOLFLGNAGTAMRSILTAATAAGNAT 119
QY 121 YVLGVPRMRERPIDGLVWGLKQADVDCLGTDCPPVRVYKIGGLPGGKVKLSGSISS 180
DB 121 YVLGVPRMRERPIDGLVWGLKQADVDCLGTDCPPVRVYKIGGLPGGKVKLSGSISS 179
QY 120 YVLGVPRMRERPIDGLVWGLKQADVDCLGTDCPPVRVYKIGGLPGGKVKLSGSISS 179
DB 120 YVLGVPRMRERPIDGLVWGLKQADVDCLGTDCPPVRVYKIGGLPGGKVKLSGSISS 179
QY 181 QYLSALMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGQ 240
DB 180 QYLSALMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGQ 239
QY 241 KYKSPKNAVVEGDASSASYFLAGAAITGGTVVEGGTTSLQGDVYKFAVLEMMGAKVTM 300
DB 240 KYKSPKNAVVEGDASSASYFLAGAAITGGTVVEGGTTSLQGDVYKFAVLEMMGAKVTM 299
QY 301 TETSVTVGPORPEPGRKHLKAIIDVNMNMPDVAMTLAVVALPADGPTAIRDVASRVKE 360
DB 300 TETSVTVGPORPEPGRKHLKAIIDVNMNMPDVAMTLAVVALPADGPTAIRDVASRVKE 359
QY 361 TERMAVIRTELTKLGASVEBGIDYCIITPPEKLVNTAIDTYDHRMAMAFSLAACADVPV 420
DB 360 TERMAVIRTELTKLGASVEBGIDYCIITPPEKLVNTAIDTYDHRMAMAFSLAACADVPV 419
QY 421 TIRDPGCTRKTPPDYFDVLSTFVKX 445
DB 420 TIRDPGCTRKTPPDYFDVLSTFVKX 444

RESULT 7
US-10-023-839-5
Sequence 5; Application US/10023839
Publication No. US20030027312A1
GENERAL INFORMATION:
APPLICANT: DEROSE, Richard
APPLICANT: CHAUBERT, Nicole
APPLICANT: GIGOT, Claude (deceased)
TITLE OF INVENTION: ISOLATED DNA SEQUENCE CAPABLE OF SERVING AS REGULATORY
TITLE OF INVENTION: ELEMENT IN A CHIMERIC GENE WHICH CAN BE USED FOR THE
TITLE OF INVENTION: TRANSFORMATION OF PLANTS
FILE REFERENCE: 022650-453
CURRENT APPLICATION NUMBER: US/10/023,839
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/000,062
PRIOR FILING DATE: EARLIER FILING DATE: 1998-05-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: FR 95/08960
PRIOR FILING DATE: EARLIER FILING DATE: 1995-07-19
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 444
TYPE: PRT
ORGANISM: Zea mays
US-10-023-839-5

Query Match 97.5%; Score 2198.5; DB 14; Length 444;
Best Local Similarity 97.5%; Pred. No. 7.8e-194;
Matches 434; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

QY 1 AGAEEVVLQPIKEISGVVYKLPKSKLSNRILLLSALAEGLTVVDNLINSEDVHYMLGALK 60
DB 1 AGAEEIVLQPIKEISGVVYKLPKSKLSNRILLLSALAEGLTVVDNLINSEDVHYMLGALK 60
QY 61 TLGLSVEADKAAKRAVAVVGGCGKFPVEKDAKEVOLFNGAGTAMRSILTAATAAGNAT 120
DB 61 TLGLSVEADKAAKRAVAVVGGCGKFPVEKDAKEVOLFNGAGTAMRSILTAATAAGNAT 120

DB 61 TLGLSVEADKAAKRAVAVVGGCGKFPVE-DAKEEVOLFLGNAGTAMRSILTAATAAGNAT 119
QY 121 YVLGVPRMRERPIDGLVWGLKQADVDCLGTDCPPVRVYKIGGLPGGKVKLSGSISS 180
DB 120 YVLGVPRMRERPIDGLVWGLKQADVDCLGTDCPPVRVYKIGGLPGGKVKLSGSISS 179
QY 181 QYLSALMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGQ 240
DB 180 QYLSALMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGQ 239
QY 241 KYKSPKNAVVEGDASSASYFLAGAAITGGTVVEGGTTSLQGDVYKFAVLEMMGAKVTM 300
DB 240 KYKSPKNAVVEGDASSASYFLAGAAITGGTVVEGGTTSLQGDVYKFAVLEMMGAKVTM 299
QY 301 TETSVTVGPORPEPGRKHLKAIIDVNMNMPDVAMTLAVVALPADGPTAIRDVASRVKE 360
DB 300 TETSVTVGPORPEPGRKHLKAIIDVNMNMPDVAMTLAVVALPADGPTAIRDVASRVKE 359
QY 361 TERMAVIRTELTKLGASVEBGIDYCIITPPEKLVNTAIDTYDHRMAMAFSLAACADVPV 420
DB 360 TERMAVIRTELTKLGASVEBGIDYCIITPPEKLVNTAIDTYDHRMAMAFSLAACADVPV 419
QY 421 TIRDPGCTRKTPPDYFDVLSTFVKX 445
DB 420 TIRDPGCTRKTPPDYFDVLSTFVKX 444

RESULT 8
US-10-869-324-5
Sequence 5; Application US/10869324
Publication No. US20050086719A1
GENERAL INFORMATION:
APPLICANT: SPENCER, MICHAEL
APPLICANT: MUMF, RITA
APPLICANT: GWYN, J. JEFFERSON
APPLICANT: MCELROY, DAVID
APPLICANT: STEPHENS, MICHAEL A.
TITLE OF INVENTION: METHOD FOR PLANT BREEDING
FILE REFERENCE: DEKM:157USC2
CURRENT APPLICATION NUMBER: US/10/869,324
CURRENT FILING DATE: 2004-06-16
PRIOR APPLICATION NUMBER: 09/698,789
PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: 08/927,368
PRIOR FILING DATE: 1997-09-11
PRIOR APPLICATION NUMBER: 08/899,247
PRIOR FILING DATE: 1997-07-23
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 570
TYPE: PRT
ORGANISM: Zea mays
US-10-869-324-5

Query Match 97.4%; Score 2196.5; DB 17; Length 570;
Best Local Similarity 97.3%; Pred. No. 1.7e-193;
Matches 433; Conservative 6; Mismatches 5; Indels 1; Gaps 1;

QY 1 AGAEEVVLQPIKEISGVVYKLPKSKLSNRILLLSALAEGLTVVDNLINSEDVHYMLGALK 60
DB 127 AGAEEIVLQPIKEISGVVYKLPKSKLSNRILLLSALAEGLTVVDNLINSEDVHYMLGALK 186
QY 61 TLGLSVEADKAAKRAVAVVGGCGKFPVEKDAKEVOLFNGAGTAMRSILTAATAAGNAT 120
DB 61 TLGLSVEADKAAKRAVAVVGGCGKFPVE-DAKEEVOLFLGNAGTAMRSILTAATAAGNAT 245
QY 121 YVLGVPRMRERPIDGLVWGLKQADVDCLGTDCPPVRVYKIGGLPGGKVKLSGSISS 180
DB 246 YVLGVPRMRERPIDGLVWGLKQADVDCLGTDCPPVRVYKIGGLPGGKVKLSGSISS 305
QY 181 QYLSALMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGQ 240
DB 181 QYLSALMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGQ 240

Db 306 QYLSALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSDRFPYIKGGQ 365
QY 241 KYKSPKNAVEGDASSASYFLAGAAITGCTVTVGCGTTSLOGDVKAETLEMMGAKVTM 300
Db 366 KYKSPKNAVEGDASSASYFLAGAAITGCTVTVGCGTTSLOGDVKAETLEMMGAKVTM 425
QY 301 TETSVTVTGPOREPFGKHLKALIDVNMNKMPPDVAMTLAVVAFADGPTAIRDVASRWYK 360
Db 426 TETSVTVTGPOREPFGKHLKALIDVNMNKMPPDVAMTLAVVAFADGPTAIRDVASRWYK 485
QY 361 TERMAVIRTELTKGASVEEGLDYCIITPPEKLVNTAIDTYDDHRMAMAFSLAACADVPV 420
Db 486 TERMAVIRTELTKGASVEEGDPYCIITPPEKLVNTAIDTYDDHRMAMAFSLAACADVPV 545
QY 421 TIRDPCTKRTKTPDPDYDVLSTFVK 445
Db 546 TIRDPCTKRTKTPDPDYDVLSTFVK 570

RESULT 9

US-11-050-645-5
; Sequence 5, Application US/11050645
; Publication No. US2005018843A1
; GENERAL INFORMATION:
; APPLICANT: SPENCER, MICHAEL
; APPLICANT: MUMM, RITA
; APPLICANT: CRYN, J. JEFFERSON
; APPLICANT: MCLENDY, DAVID
; APPLICANT: STEPHENS, MICHAEL A.
; TITLE OF INVENTION: METHOD FOR PLANT BREEDING
; FILE REFERENCE: DEK157USC2
; CURRENT APPLICATION NUMBER: US/11/050,645
; CURRENT FILING DATE: 2005-02-02
; PRIOR APPLICATION NUMBER: US/10/869,324
; PRIOR FILING DATE: 2004-06-16
; PRIOR APPLICATION NUMBER: 09/698,789
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: 08/927,368
; PRIOR FILING DATE: 1997-09-11
; PRIOR APPLICATION NUMBER: 08/899,247
; PRIOR FILING DATE: 1997-07-23
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 570
; TYPE: PRT
; ORGANISM: Zea mays
US-11-050-645-5

Query Match 97.4%; Score 2196.5; DB 20; Length 570;
Best Local Similarity 97.3%; Pred. No. 1.7e-193;
Matches 433; Conservative 6; Mismatches 5; Indels 1; Gaps 1;

QY 1 AGAEEVVLQPIKEISGVNKLPGSKLSNRILLSALAEGLTVVDNLNLSSEVDHYMGLAK 60
Db 127 AGAEEVVLQPIKEISGVNKLPGSKLSNRILLSALAEGLTVVDNLNLSSEVDHYMGLAK 186
QY 61 TLGLSEADKAKRAVAVVCGGKFPVEKDAKEEVLPLGNAGTAMRSLLTAATAAGNAT 120
Db 187 TLGLSEADKAKRAVAVVCGGKFPVE-DAKEEVLPLGNAGTAMRSLLTAATAAGNAT 245
QY 121 YVLGVPRRERIPIDLVVGLKQLGADVDCFLGTDCCPVRVVGIGLPGKVKLSGSIS 180
Db 246 YVLGVPRRERIPIDLVVGLKQLGADVDCFLGTDCCPVRVVGIGLPGKVKLSGSIS 305
QY 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSDRFPYIKGGQ 240
Db 306 QYLSALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSDRFPYIKGGQ 365
QY 241 KYKSPKNAVEGDASSASYFLAGAAITGCTVTVGCGTTSLOGDVKAETLEMMGAKVTM 300
Db 366 KYKSPKNAVEGDASSASYFLAGAAITGCTVTVGCGTTSLOGDVKAETLEMMGAKVTM 425

QY 301 TETSVTVTGPOREPFGKHLKALIDVNMNKMPPDVAMTLAVVAFADGPTAIRDVASRWYK 360
Db 426 TETSVTVTGPOREPFGKHLKALIDVNMNKMPPDVAMTLAVVAFADGPTAIRDVASRWYK 485
QY 361 TERMAVIRTELTKGASVEEGLDYCIITPPEKLVNTAIDTYDDHRMAMAFSLAACADVPV 420
Db 486 TERMAVIRTELTKGASVEEGDPYCIITPPEKLVNTAIDTYDDHRMAMAFSLAACADVPV 545
QY 421 TIRDPCTKRTKTPDPDYDVLSTFVK 445
Db 546 TIRDPCTKRTKTPDPDYDVLSTFVK 570

RESULT 10

US-09-861-696-56
; Sequence 56, Application US/09861696
; Patent No. US2002007053A1
; GENERAL INFORMATION:
; APPLICANT: Barry, Gerard F.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Padgett, Stephen R.
; APPLICANT: Stallings, William C.
; TITLE OF INVENTION: GLYPHOSATE TOLERANT 5-ENOALPYRUVYL SHIKIMATE-3-PHOSPHATE SYNTHASES
; FILE REFERENCE: 11899.0175.CNUS04 MOBT:175-4
; CURRENT APPLICATION NUMBER: US/09/861,696
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: US 09/137,440
; PRIOR FILING DATE: 1998-08-20
; PRIOR APPLICATION NUMBER: US 08/833,485
; PRIOR FILING DATE: 1997-04-07
; PRIOR APPLICATION NUMBER: US 08/306,063
; PRIOR FILING DATE: 1994-09-13
; PRIOR APPLICATION NUMBER: US 07/749,611
; PRIOR FILING DATE: 1991-08-28
; PRIOR APPLICATION NUMBER: US 07/576,537
; PRIOR FILING DATE: 1990-08-31
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 56
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Zea mays
US-09-861-696-56

Query Match 97.3%; Score 2194.5; DB 9; Length 444;
Best Local Similarity 97.3%; Pred. No. 1.8e-193;
Matches 433; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

QY 1 AGAEEVVLQPIKEISGVNKLPGSKLSNRILLSALAEGLTVVDNLNLSSEVDHYMGLAK 60
Db 1 AGAEEVVLQPIKEISGVNKLPGSKLSNRILLSALAEGLTVVDNLNLSSEVDHYMGLAK 60
QY 61 TLGLSEADKAKRAVAVVCGGKFPVEKDAKEEVLPLGNAGTAMRSLLTAATAAGNAT 120
Db 61 TLGLSEADKAKRAVAVVCGGKFPVE-DAKEEVLPLGNAGTAMRSLLTAATAAGNAT 119
QY 121 YVLGVPRRERIPIDLVVGLKQLGADVDCFLGTDCCPVRVVGIGLPGKVKLSGSIS 180
Db 120 YVLGVPRRERIPIDLVVGLKQLGADVDCFLGTDCCPVRVVGIGLPGKVKLSGSIS 179
QY 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSDRFPYIKGGQ 240
Db 180 QYLSALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSDRFPYIKGGQ 239
QY 241 KYKSPKNAVEGDASSASYFLAGAAITGCTVTVGCGTTSLOGDVKAETLEMMGAKVTM 300
Db 240 KYKSPKNAVEGDASSASYFLAGAAITGCTVTVGCGTTSLOGDVKAETLEMMGAKVTM 299
QY 301 TETSVTVTGPOREPFGKHLKALIDVNMNKMPPDVAMTLAVVAFADGPTAIRDVASRWYK 360
Db 300 TETSVTVTGPOREPFGKHLKALIDVNMNKMPPDVAMTLAVVAFADGPTAIRDVASRWYK 359
QY 361 TERMAVIRTELTKGASVEEGLDYCIITPPEKLVNTAIDTYDDHRMAMAFSLAACADVPV 420

Db 360 TERMVAIKTELTKLGASVEEGPDYCIITPEKLNVTAIIDTYDDHRMAMAFSLAACAEVAV 419
QY 421 TIRDPGCTRKTPDPYFDVLTSTFVKN 445
Db 420 TIRDPGCTRKTPDPYFDVLTSTFVKN 444

RESULT 11
US-09-464-099A-56
; Sequence 56, Application US/09464099A
; Patent No. US20020168680A1
; GENERAL INFORMATION:
; APPLICANT: Barry, Gerard F.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Padgett, Stephen R.
; APPLICANT: Stallings, William C.
; TITLE OF INVENTION: GLYHOSTE TOLERANT 5-ENOLPRUVYLSHIKIMATE-3-PHOSPHATE SYNTHASES
; FILE REFERENCE: 11899.0175.CNUS01 MOB:175-2
; CURRENT APPLICATION NUMBER: US/09/464,099A
; CURRENT FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: US 09/137,440
; PRIOR FILING DATE: 1998-08-20
; PRIOR APPLICATION NUMBER: US 08/833,485
; PRIOR FILING DATE: 1997-04-07
; PRIOR APPLICATION NUMBER: US 08/306,063
; PRIOR FILING DATE: 1994-09-13
; PRIOR APPLICATION NUMBER: US 07/749,611
; PRIOR FILING DATE: 1991-08-28
; PRIOR APPLICATION NUMBER: US 07/576,537
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 56
; LENGTH: 444
; TYPE: PRN
; ORGANISM: Zea mays
US-09-464-099A-56

Query Match 97.3%; Score 2194.5; DB 9; Length 444;
Best Local Similarity 97.3%; Pred. No. 1.8e-193;
Matches 433; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

QY 1 AGAEEVVLQPIKEISGVVKLPSSKSLSNRIILLSLAEGTTVVDNLNSEDVHYMLGALK 60
Db 1 AGAEEIVLQPIKEISGVVKLPSSKSLSNRIILLSLAEGTTVVDNLNSEDVHYMLGALK 60
QY 61 TLGLSVBADKAKRAVAVVGGCGKFPVEKDAKEVOVFLGNAGTANRSLTAATTAAGNAT 120
Db 61 TLGLSVBADKAKRAVAVVGGCGKFPVEKDAKEVOVFLGNAGTANRSLTAATTAAGNAT 119
QY 121 YVLGVPKRRERPIGDLVVGKQLGADVDCFLGTDCPPRVKVGIGLPGSKVYLSGSISS 180
Db 121 YVLGVPKRRERPIGDLVVGKQLGADVDCFLGTDCPPRVKVGIGLPGSKVYLSGSISS 179
QY 120 YVLGVPKRRERPIGDLVVGKQLGADVDCFLGTDCPPRVKVGIGLPGSKVYLSGSISS 179
Db 120 YVLGVPKRRERPIGDLVVGKQLGADVDCFLGTDCPPRVKVGIGLPGSKVYLSGSISS 179
QY 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYEMTLRMERFGVKAHSDSWDRFYIKGGQ 240
Db 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYEMTLRMERFGVKAHSDSWDRFYIKGGQ 239
QY 241 KYSPKNAVVEGDASASASYFLAGAAITGCTVVEGCGTTSLOGDVKFAVLEMMGAKVTM 300
Db 241 KYSPKNAVVEGDASASASYFLAGAAITGCTVVEGCGTTSLOGDVKFAVLEMMGAKVTM 299
QY 301 TETSVTVTGPOREPGRGHLKAIIDVNMNMMPDVAMTLAVVALPADGPTAIRVVASRWYKE 360
Db 301 TETSVTVTGPOREPGRGHLKAIIDVNMNMMPDVAMTLAVVALPADGPTAIRVVASRWYKE 359
QY 361 TERMVAIKTELTKLGASVEEGLDYCIITPEKLNVTAIIDTYDDHRMAMAFSLAACADVPV 420
Db 360 TERMVAIKTELTKLGASVEEGPDYCIITPEKLNVTAIIDTYDDHRMAMAFSLAACAEVAV 419
QY 421 TIRDPGCTRKTPDPYFDVLTSTFVKN 445

Db 420 TIRDPGCTRKTPDPYFDVLTSTFVKN 444

RESULT 12
US-10-437-963-162988
; Sequence 162988, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Bardazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 162988
; LENGTH: 515
; TYPE: PRN
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_62025C.1.pcp
US-10-437-963-162988

Query Match 96.0%; Score 2165; DB 16; Length 515;
Best Local Similarity 95.1%; Pred. No. 1.2e-190;
Matches 423; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 AGAEEVVLQPIKEISGVVKLPSSKSLSNRIILLSLAEGTTVVDNLNSEDVHYMLGALK 60
Db 71 AGAEEIVLQPIKEISGVVKLPSSKSLSNRIILLSLAEGTTVVDNLNSEDVHYMLGALK 130
QY 61 TLGLSVBADKAKRAVAVVGGCGKFPVEKDAKEVOVFLGNAGTANRSLTAATTAAGNAT 120
Db 131 ALGLSVBADKAKRAVAVVGGCGKFPVEKDAKEVOVFLGNAGTANRSLTAATTAAGNAT 190
QY 121 YVLGVPKRRERPIGDLVVGKQLGADVDCFLGTDCPPRVKVGIGLPGSKVYLSGSISS 180
Db 121 YVLGVPKRRERPIGDLVVGKQLGADVDCFLGTDCPPRVKVGIGLPGSKVYLSGSISS 250
QY 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYEMTLRMERFGVKAHSDSWDRFYIKGGQ 240
Db 251 QYLSALLMAAPLALGDVEIEIIDKLISIPYEMTLRMERFGVKAHSDSWDRFYIKGGQ 310
QY 241 KYSPKNAVVEGDASASASYFLAGAAITGCTVVEGCGTTSLOGDVKFAVLEMMGAKVTM 300
Db 311 KYSPKNAVVEGDASASASYFLAGAAITGCTVVEGCGTTSLOGDVKFAVLEMMGAKVTM 370
QY 301 TETSVTVTGPOREPGRGHLKAIIDVNMNMMPDVAMTLAVVALPADGPTAIRVVASRWYKE 360
Db 371 TETSVTVTGPOREPGRGHLKAIIDVNMNMMPDVAMTLAVVALPADGPTAIRVVASRWYKE 430
QY 361 TERMVAIKTELTKLGASVEEGLDYCIITPEKLNVTAIIDTYDDHRMAMAFSLAACADVPV 420
Db 431 TERMVAIKTELTKLGASVEEGPDYCIITPEKLNVTAIIDTYDDHRMAMAFSLAACAEVAV 490
QY 421 TIRDPGCTRKTPDPYFDVLTSTFVKN 445
Db 491 TIRDPGCTRKTPDPYFDVLTSTFVKN 515

RESULT 13
US-10-214-766-20
; Sequence 20, Application US/10214766
; Publication No. US20030084473A1
; GENERAL INFORMATION:
; APPLICANT: Gocal, Greg


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; TITLE OF INVENTION: NON-TRANSGENIC HERBICIDE RESISTANT PLANTS
; FILE REFERENCE: CA1138
; CURRENT APPLICATION NUMBER: US/10/214,766
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,734
; PRIOR FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Oryza sativa
; US-10-214-766-20

Query Match      85.5%; Score 1929; DB 14; Length 391;
Best Local Similarity 95.9%; Pred. No. 4,8e-169;
Matches 375; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 55 MLGALKTGLSVEADKAKRAVAVVCGGKFPVEKDAKEVQLFAGNAGTAMRSITAAVTA 114
D 1 MLRLKALGSLSEADKAKRAVAVVCGGKFPVEKDAKEVQLFAGNAGTAMRPLTAVTA 60
QY 115 AGGNATYVLDGVPMBRERPIGDLVVGKQAGADVCELTGDCPPVVKIGLPGSKVKL 174
D 61 AGGNATYVLDGVPMBRERPIGDLVVGKQAGADVCELTGDCPPVVKIGLPGSKVKL 120
QY 175 SSGISISQYLSALLMAAPLAGVVEIETIDCLISIPYEMTLRLMERGVKAHSDSDVDR 234
D 121 SSGISISQYLSALLMAAPLAGVVEIETIDCLISIPYEMTLRLMERGVKAHSDSDVDR 180
QY 235 YIKGGQKYSKPAKYVEGDSASVFLAGAAITGGTVEGCGTSLQGDVKEFAVLEMM 294
D 181 YIKGGQKYSKPAKYVEGDSASVFLAGAAITGGTVEGCGTSLQGDVKEFAVLEMM 240
QY 295 GAKVYTESVTVTGPREPFGKHLKAIIDVNNKMPDVAMTLAVVALPADGPTAIRDVA 354
D 241 GAKVYTESVTVTGPREPFGKHLKAIIDVNNKMPDVAMTLAVVALPADGPTAIRDVA 300
QY 355 SWEVKETERVAIRTELTKGASVEBGDVCITTPPEKLVNTAIDTYDDHRMAAFSLAA 414
D 301 SWEVKETERVAIRTELTKGASVEBGDVCITTPPEKLVNTAIDTYDDHRMAAFSLAA 360
QY 415 CADVPYTIKDPGCTRKTFPPDYFVLSYFN 445
D 361 CADVPYTIKDPGCTRKTFPPDYFVLSYFN 391

RESULT 14
US-09-861-696-55
; Sequence 55, Application US/09861696
; Patent No. US20020007053A1
; GENERAL INFORMATION:
; APPLICANT: Barry, Gerard F.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Padgett, Stephen R.
; APPLICANT: Stallings, William C.
; TITLE OF INVENTION: GLYPHOSATE TOLERANT 5-ENOALPYRUVYLSHIKIMATE-3-PHOSPHATE SYNTHASES
; FILE REFERENCE: 11899.0175.CNUS04 MOBT:175-4
; CURRENT APPLICATION NUMBER: US/09/861,696
; PRIOR APPLICATION NUMBER: US 09/137,440
; PRIOR FILING DATE: 1998-08-20
; PRIOR APPLICATION NUMBER: US 08/833,485
; PRIOR FILING DATE: 1997-04-07
; PRIOR APPLICATION NUMBER: US 08/306,063
; PRIOR FILING DATE: 1994-09-13
; PRIOR APPLICATION NUMBER: US 07/749,611
; PRIOR FILING DATE: 1991-08-28
; PRIOR APPLICATION NUMBER: US 07/576,537
; PRIOR FILING DATE: 1990-08-31
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 55

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; LENGTH: 444
; TYPE: PRT
; ORGANISM: Petunia x hybrida
; US-09-861-696-55

Query Match      85.4%; Score 1927; DB 9; Length 444;
Best Local Similarity 84.4%; Pred. No. 8,9e-169;
Matches 372; Conservative 31; Mismatches 38; Indels 0; Gaps 0;

QY 5 EVVLQPIKEISGVKLPKSKLSNRIILLALAEGLTVVDNLINSDVHYMIGALKTLGL 64
D 4 EIVLQPIKEISGVKLPKSKLSNRIILLALAEGLTVVDNLINSDVHYMIGALKTLGL 63
QY 65 SVRADKAKRAVAVVCGGKFPVEKDAKEVQLFAGNAGTAMRSITAAVTAAGNATYVD 124
D 64 HVEEDANORAAVVEGGGLPVGKESKEIQLFAGNAGTAMRPLTAATVAGNSRYVD 123
QY 125 GVPMBRERPIGDLVVGKQAGADVCELTGDCPPVVKIGLPGSKVKLSGISQYLS 184
D 124 GVPMBRERPIGDLVVGKQAGADVCELTGDCPPVVKIGLPGSKVKLSGISQYLS 183
QY 185 ALLMAAPLAGVVEIETIDCLISIPYEMTLRLMERGVKAHSDSDVDRFYIKGGQKYS 244
D 184 ALLMAAPLAGVVEIETIDCLISIPYEMTLRLMERGVKAHSDSDVDRFYIKGGQKYS 243
QY 245 PKRAYVEGDSASVFLAGAAITGGTVEGCGTSLQGDVKEFAVLEMMGAKVTTERS 304
D 244 PKRAYVEGDSASVFLAGAAITGGTVEGCGTSLQGDVKEFAVLEMMGAKVTTERS 303
QY 305 VTYVGPBPBPFGKHLKAIIDVNNKMPDVAMTLAVVALPADGPTAIRDVAAPVKTERR 364
D 304 VTYVGPBPBPFGKHLKAIIDVNNKMPDVAMTLAVVALPADGPTAIRDVAAPVKTERR 363
QY 365 VAIRTELTKGASVEBGDVCITTPPEKLVNTAIDTYDDHRMAAFSLAACADVPTIRD 424
D 364 VAIRTELTKGASVEBGDVCITTPPEKLVNTAIDTYDDHRMAAFSLAACADVPTIRD 423
QY 425 PGCTRKTFPPDYFVLSYFN 445
D 424 PGCTRKTFPPDYFVLSYFN 444

RESULT 15
US-09-464-099A-55
; Sequence 55, Application US/09464099A
; Patent No. US20020168680A1
; GENERAL INFORMATION:
; APPLICANT: Barry, Gerard F.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Padgett, Stephen R.
; APPLICANT: Stallings, William C.
; TITLE OF INVENTION: GLYPHOSATE TOLERANT 5-ENOALPYRUVYLSHIKIMATE-3-PHOSPHATE SYNTHASES
; FILE REFERENCE: 11899.0175.CNUS01 MOBT:175-2
; CURRENT APPLICATION NUMBER: US/09/464,099A
; PRIOR APPLICATION NUMBER: US 09/137,440
; PRIOR FILING DATE: 1998-08-20
; PRIOR APPLICATION NUMBER: US 08/833,485
; PRIOR FILING DATE: 1997-04-07
; PRIOR APPLICATION NUMBER: US 08/306,063
; PRIOR FILING DATE: 1994-09-13
; PRIOR APPLICATION NUMBER: US 07/749,611
; PRIOR FILING DATE: 1991-08-28
; PRIOR APPLICATION NUMBER: US 07/576,537
; PRIOR FILING DATE: 1990-08-31
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 55
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Petunia x hybrida
; US-09-464-099A-55

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Query Match 85.4%; Score 1927; DB 9; Length 444;
 Best Local Similarity 84.4%; Pred. No. 8.9e-169;
 Matches 372; Conservative 31; Mismatches 38; Indels 0; Gaps 0;

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QY      5 EVVLQPIKEISGVVVKLPGSKSLNRIILLALABGTTVDNLIINSEVDHYMLGALKTLGL 64
      11 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      4 EIVLQPIKEISGVVVKLPGSKSLNRIILLALABGTTVDNLIINSEVDHYMLGALKTLGL 63
      11 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      65 SVEADKAKRAVVVVGCGGKFPVEVDKAEVQLFIGNAGTAMRSLTAAVTAAGNATYYLD 124
      11 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      64 HVEDDSANQRAVVEGCGGLFPVGKESKEEIQLEFGNAGTAMRPLTAAVTVAGNSRYLD 123
      11 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      125 GVPRMERPIGDLVVGKQLGADVDCFLGDCPPVRVYKIGLPGGKVKLSGSISSQYLS 184
      11 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      124 GVPRMERPIGDLVVGKQLGADVDCFLGDCPPVRIVSKGGLPGGKVKLSGSISSQYLT 183
      11 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      185 ALLMAAPLALGDVEIEIIDLKLSIPYEMTLRLMERPGVKAHSDSMDRFYIKGQRYKS 244
      11 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      184 ALLMAAPLALGDVEIEIIDLKLSIPYEMTLKLMERPGISVEHSSSWDRFPVGGQRYKS 243
      11 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      245 PKNAVYEGDASSASYFLAGAAITGGTIVTEGCGTTSIQGDYKFAVYLEMMGAKVTWTETS 304
      11 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      244 PGKAPVGBDASSASYFLAGAAVVGITTVBGCCTNSIQGDYKFAVLEKMGAEVWTENS 303
      11 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      305 VTVTGQREPFGRKHLKAIDVNNMKMPDVAMTLAVVALPADGPTAIRDVASMRVKETERM 364
      11 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      304 VTVKGPPRSSSGRKHRLAIDVNNMKMPDVAMTLAVVALYADGPTAIRDVASMRVKETERM 363
      11 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      365 VAIRTELTKGASVEEGLDYCIITTPREKLVNTAIDTYDDHRMAAFSLAACADVPTIRD 424
      11 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      364 IALCTELRKLGATVEEGPDYCIITTPREKLVNTIDITYDDHRMAAFSLAACADVPTIND 423
      11 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      425 PGCTRKTFFPDYFDVLTSTFVNK 445
      11 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      424 PGCTRKTFFPDYFDVLTQYISKH 444
      11 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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Search completed: September 15, 2005, 14:10:07
 Job time : 194 secs